6 = aa 350-566
4: 1-566

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:05:49 ; Search time 23.1073 Seconds
(without alignments)
3605.942 Million cell updates/sec

Title: US-10-817-423-2
Perfect score: 4491
Sequence: 1 MRFNGKSGVEVRLPNDLEDL.....LCDGQWHSVAVSIKQRILHL 866

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3560.5	79.3	1713	2	A55347	adhesive ligand ep
2	1190	26.5	1816	1	S68960	laminin alpha-4 ch
3	948	21.1	3635	2	T10053	laminin alpha 5 ch
4	636.5	14.2	3712	2	S18253	laminin alpha-1 ch
5	600.5	13.4	3672	2	T23433	hypothetical prote
6	579.5	12.9	3704	2	T37316	probable laminin a
7	545	12.1	3084	1	MMMSA	laminin alpha-1 ch
8	531.5	11.8	1751	1	MMHUMH	laminin alpha-2 ch
9	529.5	11.8	3075	2	S14458	laminin alpha-1 ch
10	516.5	11.5	3106	1	S53868	laminin alpha-2 ch
11	358.5	8.0	3102	2	T43291	laminin alpha chai
12	321.5	7.2	1530	2	I45944	neurexin I-alpha -
13	320	7.1	1507	2	A40228	neurexin I-alpha p
14	301.5	6.7	1438	2	A48216	neurexin III-alpha
15	301.5	6.7	1471	2	B48218	neurexin III-alpha
16	301.5	6.7	1578	2	I48216	neurexin III-alpha
17	288	6.4	1715	2	C40228	neurexin II-alpha
18	261	5.8	1283	2	T13799	neurexin IV - frui
19	222.5	5.0	2823	2	F87908	protein T22A3.8 [i
20	222.5	5.0	2823	2	T23064	hypothetical prote
21	211.5	4.7	1264	2	T19545	hypothetical prote
22	195.5	4.4	3707	2	S18252	heparan sulfate pr
23	188	4.2	1722	2	E89753	protein F11C7.4 [i
24	183	4.1	1385	2	T14158	neurexin IV - mous
25	183	4.1	4391	2	A38096	perlecan precursor
26	179.5	4.0	3097	2	T00021	DN-cadherin - frui
27	174	3.9	1381	2	T31083	paranodin - rat
28	169.5	3.8	3375	2	T19821	hypothetical prote
29	168.5	3.8	882	2	A39030	androgen-binding p
30	165.5	3.7	5147	1	IJFFTM	cadherin-related t
31	164.5	3.7	402	1	BOHUS	sex steroid-bindin
32	163	3.6	403	2	A26371	sex steroid-bindin
33	163	3.6	3034	2	T14119	seven-pass transme
34	161	3.6	1959	1	AGRT	agrin - rat
35	160	3.6	2325	2	A61208	chondroitin sulfat
36	156	3.5	1193	2	T21133	hypothetical prote
37	155	3.5	1955	1	AGCH	agrin precursor -
38	154.5	3.4	367	2	A34436	sex steroid-bindin
39	149	3.3	1328	2	T43060	agrin - electric r
40	148	3.3	281	2	T33466	hypothetical prote
41	146	3.3	757	2	T34362	hypothetical prote
42	146	3.3	4307	2	T20721	hypothetical prote
43	142	3.2	1523	2	T13953	MEGF5 protein - ra
44	140	3.1	2610	2	T20968	hypothetical prote
45	138	3.1	1025	2	T42626	secreted leucine-r

ALIGNMENTS

RESULT 1
A55347
adhesive ligand epiligrin, alpha-3 chain form A precursor - human
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C;Accession: A55347
R;Ryan, M.C.; Tizard, R.; VanDevanter, D.R.; Carter, W.G.
J. Biol. Chem. 269, 22779-22787, 1994
A;Title: Cloning of the LamA3 gene encoding the alpha3 chain of the adhesive ligand epi
A;Reference number: A55347; MUID:94357926; PMID:8077230
A;Accession: A55347
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1713 <RYA>
A;Cross-references: UNIPROT:Q16787; GB:L34155; NID:g551596; PID:g551597
C;Superfamily: laminin alpha-4 chain; laminin G repeat homology; laminin-type EGF-like
C;Keywords: alternative splicing
F;67-114/Domain: laminin-type EGF-like homology <LE2>
F;1392-1534/Domain: laminin G repeat homology <LG4>

Query Match 79.3%; Score 3560.5; DB 2; Length 1713;
Best Local Similarity 78.4%; Pred. No. 1.1e-239;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||: ||||||:|||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||:: | :||||||||||: |||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||:|||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||||||:|||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:|||||||:|||:| :|  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190
```

```
Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1368

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
Db       1369 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1428

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
Db       1429 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRARAGSLPGNSTISIRAPVYL 1488

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
Db       1489 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1548

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
Db       1549 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1608

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
Db       1609 SVTPKQSLCDGQWHSVAVTIKQHILHL 1635
```

RESULT 2
S68960
laminin alpha-4 chain precursor - human
N;Alternate names: laminin Ah
C;Species: Homo sapiens (man)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: S68960; S65926; S49149; S40150; I53516
R;Richards, A.; Al-Imara, L.; Pope, F.M.
Eur. J. Biochem. 238, 813-821, 1996
A;Title: The complete cDNA sequence of laminin alpha-4 and its relationship to the other
A;Reference number: S68960; MUID:96300249; PMID:8706685
A;Accession: S68960
A;Molecule type: mRNA
A;Residues: 1-1816 <RIC>
A;Cross-references: UNIPROT:Q16363; UNIPROT:Q14731; EMBL:X91171; NID:g1212962; PIDN:CAA6
A;Experimental source: tissue type heart
R;Iivanainen, A.; Sainio, K.; Sariola, H.; Tryggvason, K.
FEBS Lett. 365, 183-188, 1995
A;Title: Primary structure and expression of a novel human laminin alpha-4 chain.
A;Reference number: I53516; MUID:95300971; PMID:7781776
A;Accession: S65926
A;Molecule type: mRNA
A;Residues: 1-142,'P',144-177,'F',179-490,'Y',492-1056,'P',1058-1816 <IIV>
A;Cross-references: EMBL:S78569; NID:g1042081; PIDN:AAB34635.1; PID:g1042082
R;Richards, A.J.; Al-Imara, L.; Carter, N.; Leversha, M.; Lloyd, J.C.; Pope, F.M.
submitted to the EMBL Data Library, December 1993
A;Description: Localisation of the gene (LAMA4) to chromosome 6q21 and isolation of a pa
A;Reference number: S49149
A;Accession: S49149
A;Molecule type: mRNA
A;Residues: 236-1816 <RI2>
A;Cross-references: EMBL:X76939; NID:g509805; PIDN:CAA54258.1; PID:g509806
R;Richards, A.J.; Al-Imara, L.; Carter, N.; Lloyd, J.C.; Pope, F.M.
submitted to the EMBL Data Library, February 1993
A;Description: Isolation of a partial cDNA encoding a protein homologous to laminin A. A
A;Reference number: S40150
A;Accession: S40150
A;Molecule type: mRNA
A;Residues: 1403-1541,'S',1543-1816 <RI3>
A;Cross-references: EMBL:X70904; NID:g437804; PIDN:CAA50261.1; PID:g437805
C;Genetics:
A;Gene: GDB:LAMA4; LAMA3
A;Cross-references: GDB:203904; OMIM:600133
A;Map position: 6q21-6q21
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin alpha-4 chain; laminin G repeat homology; laminin-type EGF-like h
C;Keywords: basement membrane; cell binding; coiled coil; extracellular matrix; glycopro
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-1816/Product: laminin alpha-4 chain #status predicted <MAT>
F;82-129/Domain: laminin-type EGF-like homology <LE1>
F;132-184/Domain: laminin-type EGF-like homology <LE2>
F;187-238/Domain: laminin-type EGF-like homology <LE3>
F;241-265/Domain: laminin-type EGF-like homology #status atypical <LE4>
F;717-719/Region: cell attachment (R-G-D) motif
F;862-1031/Domain: laminin G repeat homology <LG1>
F;1068-1223/Domain: laminin G repeat homology <LG2>
F;1252-1398/Domain: laminin G repeat homology <LG3>
F;1488-1636/Domain: laminin G repeat homology <LG4>
F;1665-1816/Domain: laminin G repeat homology <LG5>
F;104,215,308,458,524,550,571,574,631,639,735,751,754,780,803,1086,1281,1359,1411/Bindir
F;266,269/Disulfide bonds: interchain #status predicted

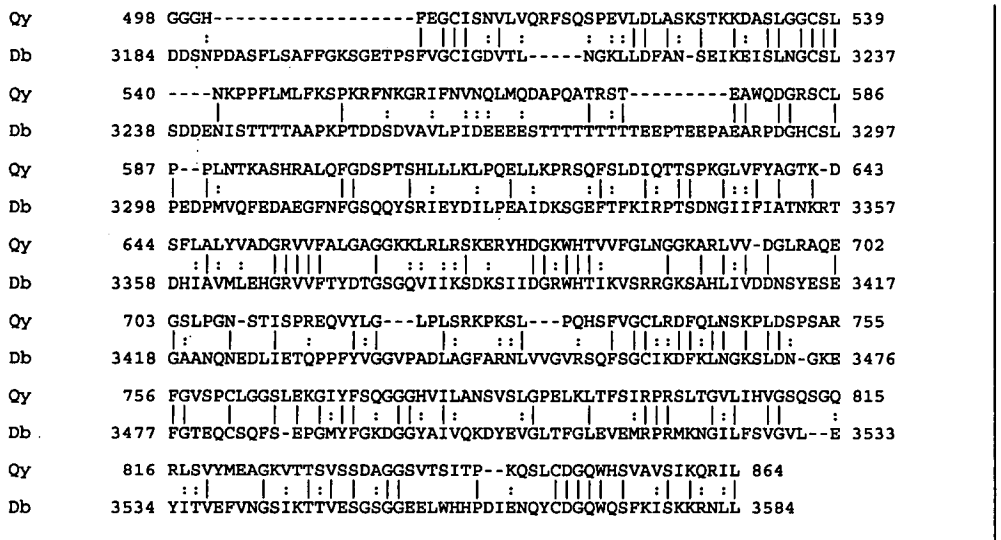
Query Match 26.5%; Score 1190; DB 1; Length 1816;
Best Local Similarity 33.2%; Pred. No. 3.6e-74;
Matches 310; Conservative 161; Mismatches 372; Indels 90; Gaps 27;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFL----QRPDLRENGGTEDMFVMYLGNKDASK 56
Db        829 MMFDGQSAVEVHSRTSMDDLKAFTSLSLYMKPPVKRPELTE---TADQFILYLGSKNAKK 885

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
Db        886 EYMGLAIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVP 943

Qy        117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDD 176
Db        944 SLSSTAEEKFIKKGEFSGDDSLLDLDPEDTVFYVGGVPSNFKLPTSLNLPGFVGCLELAT 1003

Qy        177 LNENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYA--RIPTQPN--A 227
Db       1004 LNNDVISLYNFKHIYNMDPSTSVPCARDKLAFTQSRAASYFFDGSGYAVVRDITRRGKFG 1063

Qy        228 PFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRY-------KLNSEPPKEKGI 280
Db       1064 QVTRFDIEVRTPADNGLILLMVNGSMFFRLEMRNGYLHVFYDFGFSSGRVHLEDTLKKA- 1122

Qy        281 RDTINDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIP------I 331
Db       1123 --QINDAKYHEISI-IYHNDKKMILVVDRRHVKSMDNEKMKIPFTDIYIGGAPPEILQSR 1179

Qy        332 AIRERFNISTPAFQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQM 388
Db       1180 ALRAHLPLDI-NFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQS 1236

Qy        389 SFTNLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIF 447
Db       1237 FIASIQKISFFDGFEGGFNFRTLQPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQ 1294

Qy        448 KSPGTYMDGLLHHVSVISDTSGLR--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-- 499
Db       1295 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSP 1352

Qy        500 -----GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
Db       1353 ISAQYANFTGCISNAYFTRVDRDVEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNL 1412

Qy        555 NKGRIFNVNQ--LMQDAPQATRSTEAWQDGRSCLPPLNT-----------KASHRALQF 600
Db       1413 SKPKASQNKKGGKSKDAP-------SWDPVALKLPERNTPRNSHCHLSNSPRAIEHAYQY 1465

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKD--SFLALYVADGRVVFA 658
```

```
Db       1466 GGTANSRQEFEHLKGDFGAKSQFSIRLRTRSSHGMIFYVSDQEENDFMTLFLAHGRLVYM 1525

Qy        659 LGAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSL-PGNSTISPREQV 717

Db       1526 FNVGHKKLKIRSQEKYNDGLWHDVIFIRERSSGRLVIDGLRVLEESLPPTEATWKIKGPI 1585

Qy        718 YLGLPLSRKPKSLPQ----HSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFS 773

Db       1586 YLGGVAPGKAVKNVQINSIYSFSGCLSNLQLNGASITSASQTFSVTPCFEGPMETGTYFS 1645

Qy        774 QGGGHVILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSD 833

Db       1646 TEGGYVVLDESFNIGLKFEIAFEVRPRSSSGTLVHGHSVNGEYLNVHMKNGQVIVKVNNG 1705

Qy        834 AGGSVTSITPKQSLCDGQWHSVAVSIKQRILHL 866

Db       1706 IRDFSTSVTPKQSLCDGRWHRITVIRDSNVVQL 1738


RESULT 3
T10053
laminin alpha 5 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10053
R;Miner, J.H.; Lewis, R.M.; Sanes, J.R.
submitted to the EMBL Data Library, November 1997
A;Reference number: Z16923
A;Accession: T10053
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3635 <MIN>
A;Cross-references: UNIPROT:Q61001; EMBL:U37501; NID:g2599231; PID:g2599232
C;Genetics:
A;Gene: Lama5
C;Keywords: basement membrane; cell binding; extracellular matrix
F;1888-1939/Domain: laminin-type EGF-like homology <LEG>
F;1942-1970/Domain: EGF homology <EGF>

  Query Match             21.1%;  Score 948;  DB 2;  Length 3635;
  Best Local Similarity   30.6%;  Pred. No. 8.9e-57;
  Matches  285;  Conservative  167;  Mismatches  360;  Indels  120;  Gaps   37;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGG--TEDMFVMYLGNKDASKDY 58

Db       2656 MKFNGRSGVRLRPPRDLADLAAYTALKFHIQSPVPAPEPGKNTGDHFVLYMGSRQATGDY 2715

Qy         59 IGMAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEA 117

Db       2716 MGVSLRNQKVHWVYRLGKAGPTTLSIDENIGEQ------FAAVSIDRTLQFGHMSVTVE- 2768

Qy        118 TSNKPKAPAVYDLEGGS----SNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIE 173

Db       2769 ------KQMVHEIKGDTVAPGSEGLLNLHPDDFVFYVGGYPSNFTPPEPLRFPGYLGCIE 2822

Qy        174 LDDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPNAP 228

Db       2823 METLNEEVVSLYNFEQTFMLDTAVDKPCARSKATGDPWLTDGSYLDGSGFARISFEKQ-- 2880

Qy        229 PPN---FIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPPK- 276

Db       2881 FSNTKRFDQELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFGSGLKKADPLQPPQA 2940

Qy        277 ----EKGIRDTINDGKDHSILITIGKLQKRMWINVNERSVRIEGEIFDFSTYYLGGI--- 329

Db       2941 LTAASKAIQVFLLAGNRKRVLV---RVERATVFSVDQDNML---EMAD--AYYLGGVPPE 2992

Qy        330 --PIAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSR 384

Db       2993 QLPLSLRQLFP-SGGSVRGCIKGIKALGKYVDLKRLN-TTGISFGCTADLLVGRTMTFHG 3050

Qy        385 GGQMSFTNLDV-PSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSN 443

Db       3051 HGFLPLALPDVAPITEVVYSGFGFRGTQDNNLLYYRTSPDGPYQVSLREGHVTLRFMNQE 3110

Qy        444 IPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDD--QVLRRNQRLPSFSNAQ----QSLRL 497

Db       3111 V---ETQRVFADGAPHYVAFYSNVTGVWLYVDDQLQLVKSHERTTPMLQLQPEEPSRLLL 3167

Qy        498 GG-------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKS 550

Db       3168 GGLPVSGTFHNFSGCISNVFVQRLRGPQRVFDLHQNMGSVNVSV-GCT----PAQLIETS 3222

Qy        551 PKRFNKGRIFNVNQLMQDAPQATRSTEAW-----QDGRSCLPPLNTKASHRALQF-GDSP 604

Db       3223 RATAQK-----VSRRSRQPSQDLACTTPWLPGTIQDAYQFGGPLPS-----YLQFVGISP 3272

Qy        605 TSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALGAGGK 664

Db       3273 SHRNRLHLSM-LVRPHAASQGLLLSTAP-----MSGRSPS-LVLFLNHGHFVAQTEGPGP 3325

Qy        665 KLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRA-QEGSLPGNSTISPREQVYL---- 719

Db       3326 RLQVQSRQHSRAGQWHRVSVRWGMQQIQLVVDGSQTWSQKALHHRVPRAERPQPYTLSVG 3385

Qy        720 GLPLSRKPKSLP-QHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGH 778

Db       3386 GLPASSYSSKLPVSVGFSGCLKKLQLDKQPLRTPTQMVGVTPCVSGPLEDGLFFPGSEGV 3445

Qy        779 VILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSV-YMEAGKVTTSV---SSDA 834

Db       3446 VTLELPKAKMPYVSLELEMRPLAAAGLIFHL----GQALATPYMQLKVLTEQVLLQANDG 3501

Qy        835 GGSVTSITPKQSLCDGQWHSVAVSIKQRILHL 866

Db       3502 AGEFSTWVTYPKLCDGRWHRVAVIMGRDTLRL 3533


RESULT 4
S18253
laminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C;Accession: S28399; S18253
R;Kusche-Gullberg, M.; Garrison, K.; MacKrell, A.J.; Fessler, L.I.; Fessler, J.H.
EMBO J. 11, 4519-4527, 1992
A;Title: Laminin A chain: expression during Drosophila development and genomic sequence
A;Reference number: S28399; MUID:93049203; PMID:1425586
A;Accession: S28399
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-3712 <KUS>
A;Cross-references: UNIPROT:Q00174; GB:M96388; NID:g157799; PIDN:AAA28662.1; PID:g15780
R;Garrison, K.; MacKrell, A.J.; Fessler, J.H.
J. Biol. Chem. 266, 22899-22904, 1991
A;Title: Drosophila laminin A chain sequence, interspecies comparison, and domain struc
A;Reference number: S18253; MUID:92078147; PMID:1744083
A;Accession: S18253
A;Molecule type: mRNA
A;Residues: 1762-3712 <GAR>
A;Cross-references: EMBL:M75882; NID:g157797; PIDN:AAA28661.1; PID:g157798
C;Genetics:
A;Gene: FlyBase:LanA
A;Cross-references: FlyBase:FBgn0002526
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
C;Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular
F;273-330/Domain: laminin-type EGF-like homology <LEG>
F;333-400/Domain: laminin-type EGF-like homology <LE02>
F;541-584/Domain: laminin-type EGF-like homology <LEG1>
F;1776-2115/Domain: III <DOM3>
F;1776-1806/Domain: laminin-type EGF-like homology #status atypical <LE1>
F;1809-1856/Domain: laminin-type EGF-like homology <LE2>
F;1859-1914/Domain: laminin-type EGF-like homology <LE3>
F;1917-1967/Domain: laminin-type EGF-like homology <LE4>
F;1970-2014/Domain: laminin-type EGF-like homology <LE5>
```

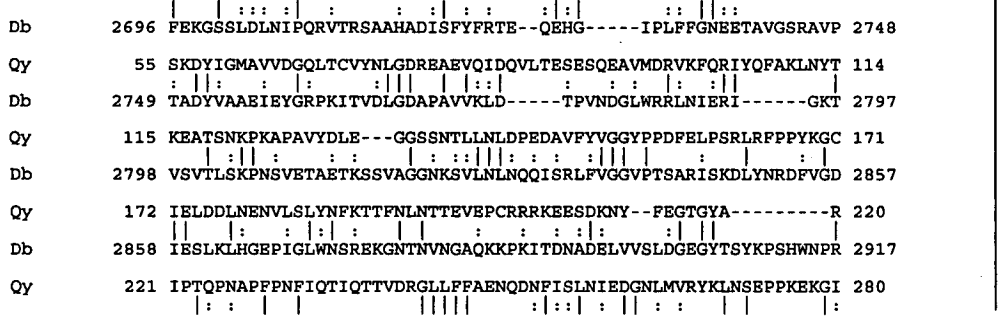
```
F;2017-2061/Domain: laminin-type EGF-like homology <LE6>
F;2064-2109/Domain: laminin-type EGF-like homology <LE7>
F;2116-2697/Domain: I/II, heptad repeats <DOM2>
F;2698-3712/Domain: G <DOMG>
F;2698-2863/Domain: repeat G1 <RG1>
F;2864-3048/Domain: repeat G2 <RG2>
F;3049-3223/Domain: repeat G3 <RG3>
F;3079-3200/Domain: laminin G repeat homology <LG3>
F;3334-3528/Domain: repeat G4 <RG4>
F;3529-3712/Domain: repeat G5 <RG5>
F;1847,1850,1943,2024,2196,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2890,2938,3

  Query Match             14.2%;  Score 636.5;  DB 2;  Length 3712;
  Best Local Similarity   24.2%;  Pred. No. 5.1e-35;
  Matches  246;  Conservative  173;  Mismatches  386;  Indels  211;  Gaps   42;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLG--NKDASK-- 56
              :|    : :|:: |    : |    |:|| : :      |  |     |::|||  || | |
Db       2675 VNFKPSTILELKTPEKTKLLATRTNLSTYFR---TTEPSG----FLLYLGNDNKTAQKNN 2727

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
              |:: : :|:|       :||:    :  |: : :    :||:||:          |||   :|
Db       2728 DFVAVEIVNGYPILTIDLGNGPERITSDKYVADGRWYQAVVDRMG-----PNAKLTIREE 2782

Qy        117 ATSNKPKAPAVYDLEGG---SSNTLLNLDPEDAVFYVGGYP--PDFELPSRLRFPPYKGC 171
                  |    : |    |  :|::|    :| |||||    ||  |  |     : |
Db       2783 L----PNGDVVEHSKSGYLEGSQNILHVDKNSRLF-VGGYPGISDFNAPPDLTTNSFSGD 2837

Qy        172 IELDDLNENVLSLYNF--KTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPF 229
              ||   : :  : |:||       :    | :    :|:       |:| || ::    |
Db       2838 IEDLKIGDESVGLWNFVYGDDNDQGARERDVLLEKKKPVTGLRFKGNGYVQLNATSNLKS 2897

Qy        230 PNFIQ---TIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTIND 286
              : ||          |||||     :::|: : || :       |       : | :|  ||
Db       2898 RSSIQFSFKADKDTSNGLLFFYGRDKHYMSIEMIDGAIFFNISLGEGGGVQSGSQDRYND 2957

Qy        287 GKDHSI---------LITIGKLQKRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERF 337
              : | :          |: :  :     |:    :  : |:       | || |      |
Db       2958 NQWHKVQAERENRNGLLKVDDIV----ISRTNAPLEADLELPKLRRLYFGGHP----RRL 3009

Qy        338 NIS---TPAFQGCMKNLKKTSGVVRLNDTV---GVTKKCSEDWKLVRTASFSRGGQMSFT 391
              | |     | | ||: |:    |||  | : |    || : ||  :  | : :     | :
Db       3010 NTSISLQPNFDGCIDNVVINQGVVDLTEYVTGGGVEEGCSAKFSTVVSYAPHEYGFLRMN 3069

Qy        392 NLDVPSTDRFQLSFGFQTFQPSGTLL---NHQTRTSSLLVTLEDGHIELSTRDSNIPIFK 448
              |  | |  :    :   |:| ||:| |     ||  ::|:: ::|:|| ::|::  | : |
Db       3070 N--VSSDNNLHVVLHFKTTQPNGVLFYAANHD-QSSTIGLSLQDGLLKLNSMGSQLVI-- 3124

Qy        449 SPGTYMDGLLH----HVSVISDTSG-LRLLIDDQVLRRNQRLPSFSNAQQSLRLGGG--- 500
                  | :|:    ||  :  | | ||| :||     |:|| |     | | | ||
Db       3125 -----DDRILNDGEDHVVTVQHTQGELRLTVDDV---DNKRLGS----PQPLILEGGDIF 3172

Qy        501 -------------------HFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNK 541
                              :| ||||:| |     : |::: |: : ||: :: ||
Db       3173 FAGLPDNYRTPRNALASLAYFVGCISDVTV-----NEEIINFANSAEKKNGNINGC---- 3223

Qy        542 PPFLMLFKS---PKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPL-------- 589
              || :: ::    |  : |     |::          |       |  | |||
Db       3224 PPHVLAYEPSLVPSYYPSGD----NEVESPWSNADTLPPLKPDIESTLPPTTPTTTTTTT 3279

Qy        590 -----NTKASHRALQPGDSP-----TSHLLLKLPQELLKPRSQFSLDI------------ 627
                  | |     ||         :  | ||::|  |    |::
Db       3280 TTTTSTTTTSTTTTTTTPSPIVIDEEKEIEAKTPQKILTTRPPAKLNLPSDERCKLPEQP 3339

Qy        628 ------------------------------------------QTTSPKGLVFYAGTK--DSF 645
                                                       :|  | ||: |||:|  | |
Db       3340 NFDVDFTEAGYRFYGLREQRLQINSLPVKVRRHHDIGISFRTERPNGLLIYAGSKQRDDF 3399

Qy        646 LALYVADGRVVFALGAGGK-KLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGS 704
              :|:|: |||| : :  | : : :: ::   :|| ||||       |  |::| |  | ||
Db       3400 IAVYLLDGRVTYEIRVGAQLQAKITTEAELNDGTWHTVEVVRTQRKVSLLIDKLE-QPGS 3458

Qy        705 LPGNS-----TISPREQVYLG---LPLSRKPKSLPQHS-----FVGCLRDFQLNSKPLDS 751
```

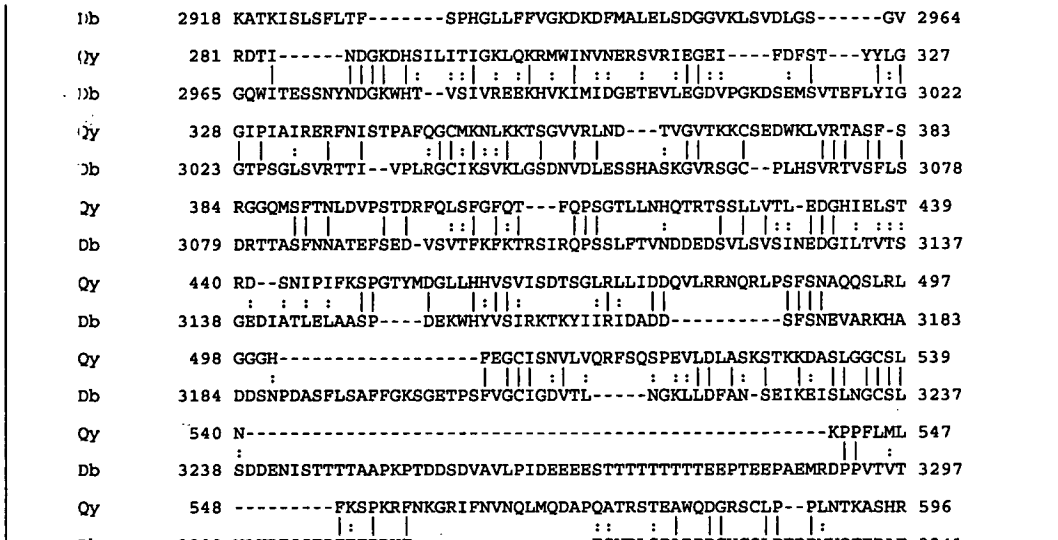
```
              :  |:      ::    :|||     |  : |:|         | |||:: : ::  |::
Db       3459 VDLNAERSAPVLAVELPIYLGGVNKFLESEVKNLTDFKTEVPYFNGCLKNIKFDAMDLET 3518

Qy        752 PSARFGVSPCLGGSLEKGIYFSQGGGHVILANSVSLGPELKLTFSIRPRSLTGVLIHVGS 811
              |   ||| ||    :|:|::|:     | : :   :| |:|::|  |||   |:|  |
Db       3519 PPEEPGVVPC-SEQVERGLFFNNQKAFVKIFDHFDVGTEMKISFDFRPRDPNGLLFSVHG 3577

Qy        812 QSGQRLSVYMEAGKVTTSVSSDAGGSVTS---ITPKQSLCDGQWHSVAVSIKQRIL 864
              ::   :   ::   :  :| :|    |::   :   :|  |||:  :|  :|| : :
Db       3578 KNSYAILELVD-NTLYFTVKTDLKNIVSTNYKLPNNESFCDGKTRNVQ-AIKSKFV 3631


RESULT 5
T23433
hypothetical protein K08C7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23433
R;Berks, M.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19740
A;Accession: T23433
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3672 <WIL>
A;Cross-references: UNIPROT:Q21313; EMBL:Z70286; PIDN:CAA94293.1; GSPDB:GN00022; CESP:K0
A;Experimental source: clone K08C7
C;Genetics:
A;Gene: CESP:K08C7.3
A;Map position: 4
A;Introns: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 3
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

  Query Match             13.4%;  Score 600.5;  DB 2;  Length 3672;
  Best Local Similarity   24.9%;  Pred. No. 1.6e-32;
  Matches  237;  Conservative  160;  Mismatches  403;  Indels  151;  Gaps   39;

Qy          3 FNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDA-------- 54
              |   | ::: :|  :      :  :| : :    :|:|       :: ||::
Db       2696 FEKGSSLDLNIPQRVTRSAAHADISFYFRTE--QEHG-----IPLFFGNEETAVGSRAVP 2748

Qy         55 SKDYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYT 114
              : ||:   :  |:     :|||  | |::|     :   : :  |:  :||          |
Db       2749 TADYVAAEIEYGRPKITVDLGDAPAVVKLD-----TPVNDGLWRRLNIERI------GKT 2797

Qy        115 KEATSNKPKAPAVYDLE---GGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGC 171
              | :|| :   : :    | : ::|||: : :  :||| |    :  |     : |
Db       2798 VSVTLSKPNSVETAETKSSVAGGNKSVLNLNQQISRLFVGGVPTSARISKDLYNRDFVGD 2857

Qy        172 IELDDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNY--FEGTGYA---------R 220
              ||   |:   : |:| :   | |      :   :  : :|:      :| ||           |
Db       2858 IESLKLHGEPIGLWNSREKGNTNVNGAQKKPKITDNADELVVSLDGEGYTSYKPSHWNPR 2917

Qy        221 IPTQPNAPFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGI 280
              |: :  |  |          |||||      :|::| : || : :   | |       |:
Db       2918 KATKISLSFLTF-------SPHGLLFFVGKDKDFMALELSDGGVKLSVDLGS------GV 2964

Qy        281 RDTI------NDGKDHSILITIGKLQKRMWINVNERSVRIEGEI----FDFST---YYLG 327
              |       |||| |:  ::| : :| : | ::  :  :||::      : |      |:|
Db       2965 GQWITESSNYNDGKWHT--VSIVREEKHVKIMIDGETEVLEGDVPGKDSEMSVTEFLYIG 3022

Qy        328 GIPIAIRERFNISTPAFQGCMKNLKKTSGVVRLND---TVGVTKKCSEDWKLVRTASF-S 383
              | |  :  |  |      :||:|::|  |  | |      : ||   |       ||| || |
Db       3023 GTPSGLSVRTTI--VPLRGCIKSVKLGSDNVDLESSHASKGVRSGC--PLHSVRTVSFLS 3078

Qy        384 RGGQMSFTNLDVPSTDRFQLSFGFQT---FQPSGTLLNHQTRTSSLLVTL-EDGHIELST 439
                  || |    | |   ::| |:|    |||     :    | | |:: ||| : :::
Db       3079 DRTTASFNNATEFSED-VSVTFKFKTRSIRQPSSLFTVNDDEDSVLSVSINEDGILTVTS 3137

Qy        440 RD--SNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQQSLRL 497
              :  : : :  ||    |  |:||:      :|:  ||          ||||
Db       3138 GEDIATLELAASP----DEKWHYVSIRKTKYIIRIDADD----------SFSNEVARKHA 3183
```



RESULT 6
T37316
probable laminin alpha chain - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37316
R;Joh, K.; Zhu, K.; Hedgecock, E.M.; Inoue, T.; Hori, K.
submitted to the EMBL Data Library, August 1998
A;Description: Laminin alpha chain gene in the nematode C. elegans.
A;Reference number: Z21681
A;Accession: T37316
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3704 <JOH>
A;Cross-references: UNIPROT:P91904; EMBL:AB016806; PIDN:BAA32347.1
A;Experimental source: strain N2
C;Genetics:
A;Gene: epi-1
A;Map position: IV
A;Introns: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 3
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match 12.9%; Score 579.5; DB 2; Length 3704;
Best Local Similarity 23.7%; Pred. No. 4.9e-31;
Matches 237; Conservative 159; Mismatches 388; Indels 215; Gaps 40;





RESULT 7
MMMSA
laminin alpha-1 chain precursor - mouse
N;Alternate names: laminin chain A1
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: A31771; A30449; S00624; A30450; S08895; S02678; S01790; A30451; S14670
R;Sasaki, M.; Kleinman, H.K.; Huber, H.; Deutzmann, R.; Yamada, Y.
J. Biol. Chem. 263, 16536-16544, 1988
A;Title: Laminin, a multidomain protein. The A chain has a unique globular domain and h
A;Reference number: A31771; MUID:89034134; PMID:3182802
A;Accession: A31771
A;Molecule type: mRNA
A;Residues: 1-3084 <SAS>
A;Cross-references: UNIPROT:P19137; EMBL:J04064; NID:g309419; PIDN:AAA39410.1; PID:g309
A;Accession: A30449
A;Molecule type: protein
A;Residues: 183-195;570-571,'A',573-586;596-612,'X',614-617,'EMK';630-646;1217-1222,'YP
2486;2624-2639;2818-2843;3009-3033,'V',3035 <SA2>
R;Hartl, L.; Oberbaeumer, I.; Deutzmann, R.
Eur. J. Biochem. 173, 629-635, 1988
A;Title: The N terminus of laminin A chain is homologous to the B chains.

A;Reference number: S00624; MUID:88225080; PMID:3267223
A;Accession: S00624
A;Molecule type: mRNA
A;Residues: 1-208,'T',210-334 <HAR>
A;Cross-references: EMBL:X07737; NID:g52857; PIDN:CAA30561.1; PID:g52858
A;Accession: A30450
A;Molecule type: protein
A;Residues: 311-335,'N',337-339;630-642,'D',644;692-734;737-748,'X',750-760,'G',762-763;
3-1389;1449-1459 <HA2>
A;Note: the sequence from Fig. 7 is inconsistent with that from Fig. 5 in having 209-Ile
R;Mann, K.; Deutzmann, R.; Timpl, R.
Eur. J. Biochem. 178, 71-80, 1988
A;Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th
A;Reference number: S08895; MUID:89078415; PMID:2462498
A;Accession: S08895
A;Molecule type: protein
A;Residues: 153-169 <MAN>
R;Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.
Biochem. J. 252, 453-461, 1988
A;Title: Structure and distribution of N-linked oligosaccharide chains on various domain
A;Reference number: S02678; MUID:88326259; PMID:2458101
A;Accession: S02678
A;Molecule type: protein
A;Residues: 630-642,'D',644;2690-2704 <FUJ>
R;Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaeumer, I.; Hartl, L.
Eur. J. Biochem. 177, 35-45, 1988
A;Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te
A;Reference number: S01790; MUID:89030693; PMID:3181157
A;Accession: S01790
A;Molecule type: mRNA
A;Residues: 2538-3084 <DEU>
A;Cross-references: EMBL:X13459; NID:g55499; PIDN:CAA31807.1; PID:g818014
A;Accession: A30451
A;Molecule type: protein
A;Residues: 1911-1929;1997-2006;2033-2045,'X',2047-2054,'X',2056-2066,'X',2068-2105;2120
470;2487-2498;2502-2525;2538-2557;2561-2591,'X',2593-2594;2600-2610;2616-2645;2648-2655;
93;2998-3005,'A',3007-3033,'V',3035;3068-3083 <DE2>
A;Note: 2256-Val was also found
R;Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
Lab. Invest. 60, 772-782, 1989
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A;Reference number: A34961; MUID:89280632; PMID:2733383
A;Accession: S14670
A;Molecule type: protein
A;Residues: 2424-2436;2440-2451;2461-2467;2487-2525;2550-2557;2561-2593;2600-2610;2616-2
-2942,'T',2944-2964;2969-2976;2980-2993;2998-3000,'I',3002-3018,'V',3020-3034;3068-3083
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-3084/Product: laminin alpha-1 chain #status predicted <MAT>
F;25-277/Domain: VI <DOM6>
F;277-331/Domain: laminin-type EGF-like homology <LE01>
F;278-519/Domain: V <DOM5>
F;334-401/Domain: laminin-type EGF-like homology <LE02>
F;404-458/Domain: laminin-type EGF-like homology <LE03>
F;461-507/Domain: laminin-type EGF-like homology <LE04>
F;510-519/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;520-715/Domain: IVb <DO4B>
F;716-1166/Domain: IIIb <DO3B>
F;716-746/Domain: laminin-type EGF-like homology #status atypical <LE06>
F;749-795/Domain: laminin-type EGF-like homology <LE07>
F;798-853/Domain: laminin-type EGF-like homology <LE08>
F;830-834/Region: cell adhesion #status predicted
F;856-906/Domain: laminin-type EGF-like homology <LE09>
F;909-955/Domain: laminin-type EGF-like homology <LE10>
F;958-1002/Domain: laminin-type EGF-like homology <LE11>
F;1005-1048/Domain: laminin-type EGF-like homology <LE12>
F;1051-1094/Domain: laminin-type EGF-like homology <LE13>
F;1097-1116/Domain: laminin-type EGF-like homology #status atypical <LE14>
F;1118-1154/Domain: laminin-type EGF-like homology #status atypical <LE15>
F;1147-1149/Region: cell attachment (R-G-D) motif
F;1157-1166/Domain: laminin-type EGF-like homology #status atypical <LE16>
F;1167-1368/Domain: IVa <DO4A>
F;1369-1561/Domain: IIIa <DO3A>
F;1369-1407/Domain: laminin-type EGF-like homology #status atypical <LE17>
F;1410-1456/Domain: laminin-type EGF-like homology <LE18>
F;1459-1513/Domain: laminin-type EGF-like homology <LE19>
F;1516-1560/Domain: laminin-type EGF-like homology <LE20>
F;1562-2133/Domain: II/I <DOM2>
F;1562-2133/Region: heptad repeats
F;2134-3084/Domain: G <DOMG>
F;2150-2308/Domain: laminin G repeat homology <LG1>
F;2337-2492/Domain: laminin G repeat homology <LG2>
F;2518-2683/Domain: laminin G repeat homology <LG3>
F;2748-2897/Domain: laminin G repeat homology <LG4>
F;2925-3082/Domain: laminin G repeat homology <LG5>
F;25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;45,79,370,374,531,562,672,808,914,959,969,1052,1344,1414,1586,1603,1659,1686,1706,1718
e (Asn) (covalent) #status predicted
F;304-312/Disulfide bonds: #status experimental
F;770,857,1999,2055,2067,2835/Binding site: carbohydrate (Asn) (covalent) #status experi
F;845,2102/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 12.1%; Score 545; DB 1; Length 3084;
Best Local Similarity 21.6%; Pred. No. 9.2e-29;
Matches 212; Conservative 171; Mismatches 372; Indels 226; Gaps 36;

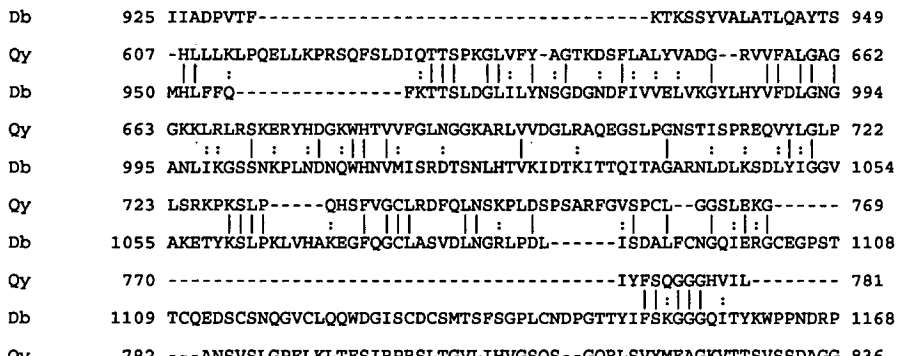
```
Qy          7 SGVEVRLPNDLEDLKGY---TS--------LSLFLQRPDLRENGGTEDMFVMYLGNKDAS 55
              : ::| :  | : :: |   ||         |::  | |          |  : |||:  :|
Db       2122 ASIKVAVSADRDCIRAYQPQTSSTNYNTLILNVKTQEP---------DNLLFYLGS-SSS 2171

Qy         56 KDYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLN--Y 113
               |:: : :  |::  :::||      ::  :|   :    ::         | :|  :
Db       2172 SDFLAVEMRRGKVAFLWDLGSGSTRLEFPEVSINNNRWHSIY-------ITRFGNMGSLS 2224

Qy        114 TKEA---------TSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLR 164
               |||          ||  |     | |:   :::||:          :|||     :    ::
Db       2225 VKEASAAENPPVRTSKSPGPSKVLDI---NNSTLM---------FVGGLGGQIKKSPAVK 2272

Qy        165 FPPYKGCIELDDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNY-FEGTGYARIPT 223
              :|||:    ||   : |:|:          :   |    :  | :: |:|:||| :
Db       2273 VTHFKGCMGEAFLNGKSIGLWNYIE----REGKCNGCFGSSQNEDSSFHFDGSGYAMVEK 2328

Qy        224 QPNAPFPNFIQTIQTTVDRGLLFF--AENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIR 281
                  :    |   ||||:  :    :|:|: :  | : |   | | |
Db       2329 TLRPTVTQIVILFSTFSPNGLLFYLASNGTKDFLSIELVRGRVKVMVDLGSGP------- 2381

Qy        282 DTINDGKDHSILITIGKLQKRMWINVNERSVRIEGEIFDFSTY---------------- 324
                  |:|  :      |  :  :  | :| :  | |
Db       2382 ---------LTLMTDRRYNNGTWYKIAFQRNRKQGLLAVFDAYDTSDKETKQGETPGAAS 2432

Qy        325 ----------YLGGIPIAIRERFNISTPAFQGCMKNLK-KTSGVVRLNDTVGVTKKCSED 373
                       |:||:| :   |  :|: :: ||:|||:   |    | :: || | |:
Db       2433 DLNRLEKDLIYVGGLPHSKAVRKGVSSRSYVGCIKNLEISRSTFDLLRNSYGVRKGCA-- 2490

Qy        374 WKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLL-NHQTRTSS--LLVTL 430
               : ::: || |||      :::|           ::  |  :||    |: ||  ||| |
Db       2491 LEPIQSVSFLRGGY-----VEMPP----------KSLSPESSLLATFATKNSSGILLVAL 2535

Qy        431 EDGHIELSTRDSNIPIFK-------------------------SPGTYMDGLLHHVSV 463
                  |    :::| |                          |:| ||  | :|:
Db       2536 GKDAEEAGGAQAHVPFFSIMLLEGRIEVHVNSGDGTSLRKALLHAPTGSYSDGQEHSISL 2595

Qy        464 ISDTSGLRLLIDDQVLRRNQRLPSFSNAQQSLRLG--------------GG-------- 500
               : :   : : :|:             |:  ::||              ||
Db       2596 VRNRRVITIQVDE------------NSPVEMKLGPLTEGKTIDISNLYIGGLPEDKATP 2642

Qy        501 ------HFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
                   | ||| ||::       ::||    :  :   |  | | : |   | :
Db       2643 MLKMRTSFHGCIKNVVL-----DAQLLDFTHATGSEQVELDTCLLAEEPMQSLHREH--- 2694

Qy        555 NKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQFGDSPTSHLLLKLPQ 614
                    :|  : |   :      |      |     :|   ||| |  |||:| | |
```

```
Db       2695 --------GELPPEPPTLPQPELCAVD----TAPGYVAGAH---QFGLSQNSHLVLPLNQ 2739

Qy        615 ELLKPRSQFSLDIQTTSPKGLVFYAGTKD--SFLALYVADGRVVFALGAGGKKLRLRSKE 672
              . :: | |  | |:| :  ||::|   ::   :  | : :||: |    |  : ::
Db       2740 SDVRKRLQVQLSIRTFASSGLIYYVAHQNQMDYATLQLQEGRLHFMFDLGKGRTKVSHPA 2799

Qy        673 RYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGN-STISPREQVYL-GLPLSRKPKSL 730
                 |||||||        || : |||  :   :: || :|:    ::|| |||   : :::
Db       2800 LLSDGKWHTVKTEYIKRKAFMTVDGQESPSVTVVGNATTLDVERKLYLGGLPSHYRARNI 2859

Qy        731 P--QHSFVGCLRDFQLNSKPLDS--PSARFGVSPCLGGSLEKGIYFSQGGGHVILANSVS 786
              ||   |: :  :| : ||   | :   |  |   : ::| :|    |  ::
Db       2860 GTITHSIPACIGEIMVNGQQLDKDRPLSASAVDRCYVVA-QEGTFFEGSGYAALVKEGYK 2918

Qy        787 LGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTSITPK-- 844
              :  :| :|   |  |  |||: : |     : : :  |||   |:: ||    :  |:
Db       2919 VRLDLNITLEFRTTSKNGVLLGISSAKVDAIGLEIVDGKVLFHVNNGAGRITATYQPRAA 2978

Qy        845 QSLCDGQWHSV-AVSIKQRIL 864
              ::||||:||:: |   | ||:
Db       2979 RALCDGKWHTLQAHKSKHRIV 2999


RESULT 8
MMHUMH
laminin alpha-2 chain - human (fragment)
N;Alternate names: laminin M chain; merosin heavy chain
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: PX0082; A35899; A38970; S14461
R;Hori, H.; Kanamori, T.; Mizuta, T.; Yamaguchi, N.; Liu, Y.; Nagai, Y.
J. Biochem. 116, 1212-1219, 1994
A;Title: Human laminin M chain: Epitope analysis of its monoclonal antibodies by immunos
A;Reference number: PX0082; MUID:95221315; PMID:7535762
A;Accession: PX0082
A;Molecule type: mRNA
A;Residues: 1-1751 <HOR>
A;Cross-references: UNIPROT:P24043
A;Experimental source: placenta
R;Ehrig, K.; Leivo, I.; Argraves, W.S.; Ruoslahti, E.; Engvall, E.
Proc. Natl. Acad. Sci. U.S.A. 87, 3264-3268, 1990
A;Title: Merosin, a tissue-specific basement membrane protein, is a laminin-like protein
A;Reference number: A35899; MUID:90238994; PMID:2185464
A;Accession: A35899
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 'V',623-1751 <EHR1>
A;Cross-references: EMBL:M59832
A;Accession: A38970
A;Molecule type: protein
A;Residues: 1368-1384;1389-1406;1593-1607 <EHR2>
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in lacking 1599-V
R;Ehrig, K.; Leivo, I.; Argraves, S.W.; Ruoslahti, E.; Engvall, E.
submitted to the EMBL Data Library, December 1990
A;Description: The tissue-specific basement membrane protein merosin is a laminin-like p
A;Reference number: S14461
A;Accession: S14461
A;Molecule type: mRNA
A;Residues: 'V',623-1264,'R',1266-1751 <LEI>
A;Cross-references: EMBL:M59832; NID:g187520; PIDN:AAA63215.1; PID:g187521
C;Comment: This protein is a prominent component of the basement membrane that mediates
C;Genetics:
A;Gene: GDB:LAMA2; LAMM
A;Cross-references: GDB:132362; OMIM:156225
A;Map position: 6q22-6q23
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C;Keywords: basement membrane; calcium binding; coiled coil; extracellular matrix; glyco
F;21-58/Domain: laminin-type EGF-like homology #status atypical <LE01>
F;61-107/Domain: laminin-type EGF-like homology <LE02>
F;110-165/Domain: laminin-type EGF-like homology <LE03>
F;168-212/Domain: laminin-type EGF-like homology <LE04>
F;527-567,1071-1300/Region: 3DM and 2D9 binding
F;811-972/Domain: laminin G repeat homology <LG1>
F;1005-1165/Domain: laminin G repeat homology <LG2>
F;1191-1354/Domain: laminin G repeat homology <LG3>
F;1430-1578/Domain: laminin G repeat homology <LG4>
F;1605-1751/Domain: laminin G repeat homology <LG5>
F;120,238,255,341,451,542,557,561,658,669,686,767,881,1001,1076,1119,1192,1199,1289,150

  Query Match           11.8%;  Score 531.5;  DB 1;  Length 1751;
  Best Local Similarity  24.1%;  Pred. No. 3.1e-28;
  Matches  225;  Conservative  161;  Mismatches  360;  Indels  187;  Gaps   44;

Qy         43 DMFVMYLGNKDASK--DYIGMAVVDGQLTCVYNLGDREAEVQI-DQVLTESESQEAVMDR 99
              |  : |||   ::|  |:: : :  |::: ::::|      |:  |  : :|      |  |
Db        821 DNLLFYLG---SAKFIDFLAIEMRKGKVSFLWDVGSGVGRVEYPDLTIDDSYWYRIVASR 877

Qy        100 VKFQRIYQFAKLNYTKEATSNKPKA---PAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPD 156
                        |        : |||   |: :        |:|::|  :|: :|||
Db        878 TGRNGTISVRAL--------DGPKASIVPSTHHSTSPPGYTILDVD-ANAMLFVGGLTGK 928

Qy        157 PELPSRLRFPPYKGCIELDDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKN---YF 213
               :   :|  : ||:     :   : |:||:        : : |    :  |       |
Db        929 LKKADAVRVITFTGCMGETYFDNKPIGLWNFRE----KEGDCKGCTVSPQVEDSEGTIQF 984

Qy        214 EGTGYARIPTQPNAPFPNFIQTI----QTTVDRGLLFFAENQD--NFISLNIEDGNLMVR 267
              :| ||| : ::|   :|| | |:    :|     || :   :|  :|:|: : ||:: |
Db        985 DGEGYALV-SRPIRWYPN-ISTVMFKFRTFSSSALLMYLATRDLRDFMSVELTDGHIKVS 1042

Qy        268 YKLNSEPPKEKGIRDTI-----NDGKDHSILITIGKLQKRMWINVNERSVRIEGEIFDFS 322
              | | |       |:   :      ||||  |    |: ::||:  |:: :      |  |   |
Db       1043 YDLGS------GMASVVSNQNHNDGKWKS--FTLSRIQKQANISIVDIDTNQEENIATSS 1094

Qy        323 T------------YYLGGIP----IAIRERFNISTPAFQGCMKNL---KKTSGVVRLND 362
              :                | ||:|    :::: |  ::   : ||:|::    :    ::   |
Db       1095 SGNNFGLDLKADDKIYFGGLPTLRNLSMKARPEVNLKKYSGCLKDIEISRTPYNILSSPD 1154

Qy        363 TVGVTKKCSEDWKLVRTASFSRGG--QMSFTNLDVPSTDRFQLSFGFQTFQPSGTLL--- 417
              ||||| ||   : | | || : |  ::|   :|| :    :::  | |    || :|
Db       1155 YVGVTKGCS--LENVYTVSFPKPGFVELSPVPIDVGT----EINLSFSTKNESGIILLGS 1208

Qy        418 ----------NHQTRTSSLLVTLEDGHIE--LST---RDSNIPIFKSPGTYMDGLLHHVS 462
                       ||  :  :: |  | :|  |||       | |   |  : ||  | |
Db       1209 GGTPAPPRRKRRQTGQAYYVILLNRGRLEVHLSTGARTMRKIVIRPEPNLFHDGREHSVH 1268

Qy        463 VISDTSGLRLLIDDQVLRRNQRLPSFSNAQ-QSLRLGGG------------HFEGCISN 508
              |   | |:  :  |:  | | |       : : | :||              |||| |
Db       1269 V-ERTRGIFTVQVDENRRYMQNLTVEQPIEVKKLFVGGAPPEFQPSPLRNIPPFEGCIWN 1327

Qy        509 VLVQRFSQSPEVLDLASKSTKKDASLGGCSLNK---------PPFLML---------FKS 550
              :::         :| |  : |:| :| |:  |         |  :::          | :
Db       1328 LVINSVP-----MDFARPVSFKNADIGRCAHQKLREDEDGAAPAEIVIQPEPVPTPAPPT 1382

Qy        551 PKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQFGDSPTSHLLL 610
              |                ::   | | |  |   |               : ||| |  ||: :
Db       1383 P-----------TPVLTHGPCAAESEPALLIG-------------SKQFGLSRNSHIAI 1417

Qy        611 KLPQELLKPRSQFSLDIQTTSPKGLVFYAG--TKDSFLALYVADGRVVFA--LGAGGKKL 666
                 :| |   |:::| :  ||:||       |  : : :|   |:  ||:|
Db       1418 AFDDTKVKNRLTIELEVRTEAESGLLFYMARINHADFATVQLRNGLPYFSYDLGSGDTHT 1477

Qy        667 RLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPRE--------QVY 718
              : :|   :||:|| :    :  | |||          | ||||::         :|
Db       1478 MIPTK--INDGQWHKIKIMRSKQEGILYVDG--------ASNRTISPKKADILDVVGMLY 1527

Qy        719 L-GLPLSRKPKSL--PQHSFVGCLRDFQLNSKP--LDSPSARFGVSPCLGGSLEKGIYFS 773
              : |||::   : :    :|  ||:|:  :   |  |: |:: | |  |   : ::| ||
Db       1528 VGGLPINYTTRRIGPVTYSIDGCVRNLHMAEAPADLEQPTSSFHVGTCFANA-QRGTYF- 1585

Qy        774 QGGGHVILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSD 833
              | |          :| :| : |  | : ||||: : ||    : : |   |:    | :
Db       1586 DGTGFAKAVGGFKVGLDLLVEFEFRTTTTTGVLLGISSQKMDGMGIEMIDEKLMFHVDNG 1645
```

```
Qy        834 AG--GSVTSITPKQSLCDGQWHSV-AVSIKQRI 863
              ||   :|        |||||| | |  || ||
Db       1646 AGRFTAVYDAGVPGHLCDGQWHKVTANKIKHRI 1678


RESULT 9
S14458
laminin alpha-1 chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S14458; S14663; A34961
R;Haaparanta, T.; Uitto, J.; Ruoslahti, E.; Engvall, E.
Matrix 11, 151-160, 1991
A;Title: Molecular cloning of the cDNA encoding human laminin A chain.
A;Reference number: S14458; MUID:91333420; PMID:1714537
A;Accession: S14458
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-3075 <HAA>
A;Cross-references: UNIPROT:P25391
R;Nissinen, M.; Vuolteenaho, R.; Boot-Handford, R.; Kallunki, P.; Tryggvason, K.
Biochem. J. 276, 369-379, 1991
A;Title: Primary structure of the human laminin A chain. Limited expression in human tis
A;Reference number: S14663; MUID:91264789; PMID:2049067
A;Accession: S14663
A;Molecule type: mRNA
A;Residues: 1-227,'FE',230-251,'MLP',255-418,'E',420-518,'L',520-1022,'V',1024-1074,'V',
A;Cross-references: EMBL:X58531; NID:g34225; PIDN:CAA41418.1; PID:g34226
R;Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
Lab. Invest. 60, 772-782, 1989
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A;Reference number: A34961; MUID:89280632; PMID:2733383
A;Accession: A34961
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 'W',2397-2745,'L',2747-3053,'L',3055-3072,'PSP' <OLS>
A;Note: the authors translated the codon AGA for residue 2692 as Pro
C;Genetics:
A;Gene: GDB:LAMA1; LAMA
A;Cross-references: GDB:120135; OMIM:150320
A;Map position: 18p11.32-18p11.22
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; disulfide bon
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-3075/Product: laminin alpha-1 chain #status predicted <MAT>
F;18-269/Domain: VI <DOM6>
F;270-516/Domain: V <DOM5>
F;270-324/Domain: laminin-type EGF-like homology <LE1>
F;327-394/Domain: laminin-type EGF-like homology <LE2>
F;397-451/Domain: laminin-type EGF-like homology <LE3>
F;454-500/Domain: laminin-type EGF-like homology <LE4>
F;503-512/Domain: laminin-type EGF-like homology #status atypical <LE5>
F;517-708/Domain: IVb <DO4B>
F;709-1159/Domain: IIIb <DO3B>
F;709-739/Domain: laminin-type EGF-like homology #status atypical <LE6>
F;742-788/Domain: laminin-type EGF-like homology <LE7>
F;791-846/Domain: laminin-type EGF-like homology <LE8>
F;849-899/Domain: laminin-type EGF-like homology <LE9>
F;902-948/Domain: laminin-type EGF-like homology <LE10>
F;951-995/Domain: laminin-type EGF-like homology <LE11>
F;998-1041/Domain: laminin-type EGF-like homology <LE12>
F;1044-1087/Domain: laminin-type EGF-like homology <LE13>
F;1090-1109/Domain: laminin-type EGF-like homology #status atypical <LE14>
F;1111-1147/Domain: laminin-type EGF-like homology #status atypical <LE15>
F;1150-1159/Domain: laminin-type EGF-like homology #status atypical <LE16>
F;1160-1361/Domain: IVa <DO4A>
F;1362-1553/Domain: IIIa <DO3A>
F;1362-1400/Domain: laminin-type EGF-like homology #status atypical <LE17>
F;1403-1449/Domain: laminin-type EGF-like homology <LE18>
F;1452-1506/Domain: laminin-type EGF-like homology <LE19>
F;1509-1553/Domain: laminin-type EGF-like homology <LE20>
F;1554-2125/Domain: I/II, heptad repeats <DOM2>
F;2116-2120/Region: cell adhesion #status predicted
F;2126-3075/Domain: G <DOMG>
F;2142-2300/Domain: laminin G repeat homology <LG1>
F;2329-2484/Domain: laminin G repeat homology <LG2>
F;2510-2676/Domain: laminin G repeat homology <LG3>
F;2534-2536/Region: cell attachment (R-G-D) motif
F;2739-2888/Domain: laminin G repeat homology <LG4>
F;2916-3073/Domain: laminin G repeat homology <LG5>
F;38,164,555,665,763,801,838,926,952,1045,1407,1579,1596,1678,1689,1698,1717,1804,1894,1
rate (Asn) (covalent) #status predicted
F;297-305/Disulfide bonds: #status predicted

  Query Match            11.8%;  Score 529.5;  DB 2;  Length 3075;
  Best Local Similarity  22.4%;  Pred. No. 1.1e-27;
  Matches  211;  Conservative  175;  Mismatches  403;  Indels  155;  Gaps   36;

Qy          7 SGVEVRLPNDLEDLKGY----------TSLSLFLQRPDLRENGGTEDMFVMYLGNKDAS 55
              : ::| :  | : :: |           :|::  | |          |  : |||:  ||
Db       2114 ASIKVAVSADRDCIRAYQPQISSTNYNTLTLNVKTQEP---------DNLLFYLGSSTAS 2164

Qy         56 KDYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLN--Y 113
               |:: : :  |::  :::||      ::       :     ::        : :|  :
Db       2165 -DFLAVEMRRGRVAFLWDLGSGSTRLEFPDFPIDDNRWHSI-------HVARFGNIGSLS 2216

Qy        114 TKEATSNKPKAPAVYDLEGGSSNTL-LNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCI 172
              || :||: |:|       |::| | :|      : :|||     :    ::   :|||:
Db       2217 VKEMSSNQ-KSPTKTSKSPGTANVLDVN---NSTLMFVGGLGGQIKKSPAVKVTHFKGCL 2272

Qy        173 ELDDLNENVLSLYNFKTTFNLNTTEVE-PCR----RRKEESDKNYFEGTGYARIPTQPNA 227
                ||   : |:|:       | |  ||      : |    :|:|:||: :     |
Db       2273 GEAFLNGKSIGLWNY--------IEREGKCRGCFGSSQNEDPSFHFDGSGYSVVEKSLPA 2324

Qy        228 PFPNFIQTIQTTVDRGLLFF--AENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTIN 285
                |    |    ||| :  :    :|:|: :  | : |   | | |      |   |
Db       2325 TVTQIIMLFNTFSPNGLLLYLGSYGTKDFLSIELFRGRVKVMTDLGSGPITLLTDR-RYN 2383

Qy        286 DGKDHSILITIGKLQKRMWI----NVNERSVRIEGEI---------FDFSTYYLGGIPIA 332
              :|  : |     : |  : :    | : :  : :||           |    |:||:| :
Db       2384 NGTWYKIAFQRNRKQGVLAVIDAYNTSNKETK-QGETPGASSDLNRLDKDPIYVGGLPRS 2442

Qy        333 IRERFNISTPAFQGCMKNLK-KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFT 391
              |  ::| :| ||:|||:    |    | :: || | |    : :|: || :|| :
Db       2443 RVVRRGVTTKSFVGCIKNLEISRSTFDLLRNSYGVRKGCL--LEPIRSVSFLKGGYIELP 2500

Qy        392 NLDVPSTDRFQLSFGFQTFQPSGTLL-----------NHQTRTSSLLVTLEDGHIELST 439
              :     : ::|   |   || :|              :       | |  |:||:
Db       2501 PKSLSPESEWLVTFA--TTNSSGIILAALGGDVEKRGDREEAHVPFFSVMLIGGNIEVHV 2558

Qy        440 RDSN-----IPIFKSP-GTYMDGLLHHVSVISDTSGLRLLIDDQ---VLRRNQRLPSFSN 490
              :       :  :| || ||  | :|:: :   : : :|:      ::    : | :
Db       2559 NPGDGTGLRKALLHAPTGTCSDGQAHSISLVRNRRIITVQLDENNPVEMKLGTLVESRTI 2618

Qy        491 AQQSLRLGG-------------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGC 537
              :| :||              | ||| |::      : |:||  |   :   |  |
Db       2619 NVSNLYVGGIPEGEGTSLLTMRRSFHGCIKNLIF-----NLELLDFNSAVGHEQVDLDTC 2673

Qy        538 SLNKPPFL-------MLFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLN 590
              |:: | |         | : |: | :  :  |:  ::  | |
Db       2674 WLSERPKLAPDAEDSKLLREPRAFPEQCV--VDAALEYVPGA------------------ 2713

Qy        591 TKASHRALQFGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKD--SFLAL 648
                |  ||| :  || :|   |  :: :    | |:| :  ||::|   ::   :  |
Db       2714 ----H---QFGLTQNSHFILPFNQSAVRKKLSVELSIRTFASSGLIYYMAHQNQADYAVL 2766

Qy        649 YVADGRVVFALGAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGN 708
              :  ||: |    |  : ::       |||||||       |  : |||  :   :: |:
Db       2767 QLHGGRLHFMFDLGKGRTKVSHPALLSDGKWHTVKTDYVKRKGFITVDGRESPMVTVVGD 2826

Qy        709 STISPREQVYL--GLPLSRKPKSLPQ--HSFVGCLRDFQLNSKPL--DSPSARFGVSPCL 762
              |:   | ::   |||   : : :    ||    |: |  :||| |  ||| : | |: |
Db       2827 GTMLDVEGLFYLGGLPSQYQARKIGNITHSIPACIGDVTVNSKQLDKDSPVSAFTVNRCY 2886

Qy        763 GGSLEKGIYFSQGGGHVILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYME 822
                : ::| ||   |   ::     :  :: :|   |  |  |||: : :     : : :
```

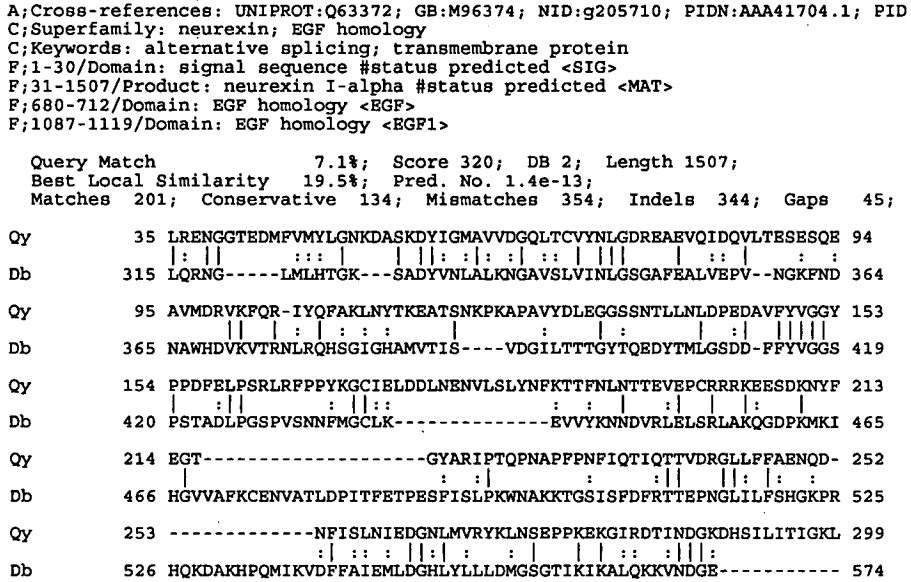
```
Db       2887 AVA-QEGTYFDGSGYAALVKEGYKVQSDVNITLEFRTSSQNGVLLGISTAKVDAIGLELV 2945

Qy        823 AGKVTTSVSSDAGGSVTSITPKQS--LCDGQWHSV-AVSIKQRI 863
              |||   |:: ||    :  || :  ||||:||:: |   | ||
Db       2946 DGKVLFHVNNGAGRITPAYEPKTATVLCDGKWHTLQANKSKHRI 2989


RESULT 10
S53868
laminin alpha-2 chain precursor - mouse
N;Alternate names: laminin M chain; merosin heavy chain
C;Species: Mus musculus (house mouse)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: I49077; S50829; I48655; S31576; S53868
R;Bernier, S.M.; Utani, A.; Sugiyama, S.; Doi, T.; Polistina, C.; Yamada, Y.
Matrix Biol. 14, 447-455, 1995
A;Title: Cloning and expression of laminin alpha 2 chain (M-chain) in the mouse.
A;Reference number: I49077; MUID:95316259; PMID:7795883
A;Accession: I49077
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3106 <RES>
A;Cross-references: UNIPROT:Q60675; EMBL:U12147; NID:g699109; PIDN:AAC52165.1; PID:g6991
R;Xu, H.; Wu, X.R.; Wewer, U.M.; Engvall, E.
Nature Genet. 8, 297-302, 1994
A;Title: Murine muscular dystrophy caused by a mutation in the laminin alpha-2 (Lama2) g
A;Reference number: S50829; MUID:95179178; PMID:7874173
A;Accession: S50829
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 64-281 <XUH>
A;Cross-references: GB:S75315; NID:g833929; PIDN:AAB33573.1; PID:g833930
R;Chang, A.C.; Wadsworth, S.; Coligan, J.E.
J. Immunol. 151, 1789-1801, 1993
A;Title: Expression of merosin in the thymus and its interaction with thymocytes.
A;Reference number: I48655; MUID:93346725; PMID:8345183
A;Accession: I48655
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 2162-2204,'D',2206-2213,'EY',2216-2279 <RE2>
A;Cross-references: EMBL:X69869; NID:g53055; PIDN:CAA49502.1; PID:g53056
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C;Keywords: basement membrane; calcium binding; coiled coil; extracellular matrix; glycc
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-3106/Product: laminin alpha-2 chain #status predicted <MAT>
F;283-337/Domain: laminin-type EGF-like homology <LE01>
F;340-407/Domain: laminin-type EGF-like homology <LE02>
F;410-462/Domain: laminin-type EGF-like homology <LE03>
F;465-511/Domain: laminin-type EGF-like homology <LE04>
F;514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;720-750/Domain: laminin-type EGF-like homology <LE06>
F;753-800/Domain: laminin-type EGF-like homology <LE07>
F;803-858/Domain: laminin-type EGF-like homology <LE08>
F;861-911/Domain: laminin-type EGF-like homology <LE09>
F;914-960/Domain: laminin-type EGF-like homology <LE10>
F;963-1007/Domain: laminin-type EGF-like homology <LE11>
F;1010-1053/Domain: laminin-type EGF-like homology <LE12>
F;1056-1099/Domain: laminin-type EGF-like homology <LE13>
F;1102-1121/Domain: laminin-type EGF-like homology #status atypical <LE14>
F;1123-1159/Domain: laminin-type EGF-like homology #status atypical <LE15>
F;1162-1171/Domain: laminin-type EGF-like homology #status atypical <LE16>
F;1376-1413/Domain: laminin-type EGF-like homology #status atypical <LE17>
F;1416-1462/Domain: laminin-type EGF-like homology <LE18>
F;1465-1520/Domain: laminin-type EGF-like homology <LE19>
F;1523-1567/Domain: laminin-type EGF-like homology <LE20>
F;2166-2327/Domain: laminin G repeat homology <LG1>
F;2360-2520/Domain: laminin G repeat homology <LG2>
F;2546-2709/Domain: laminin G repeat homology <LG3>
F;2785-2933/Domain: laminin G repeat homology <LG4>
F;2960-3106/Domain: laminin G repeat homology <LG5>

 Query Match           11.5%;  Score 516.5;  DB 1;  Length 3106;
 Best Local Similarity  23.2%;  Pred. No. 9.1e-27;
 Matches  220;  Conservative  169;  Mismatches  375;  Indels  183;  Gaps   46;

Qy         32 RPDLRENG----------GTEDMFVMYLGNKDASK--DYIGMAVVDGQLTCVYNLGDREA 79
              ||::::               |  : |||   ::|  |:: : :  |::: :: :|
Db       2155 RPEIKKGSYNNIVVHVKTAVADNLLFYLG---SAKFIDFLAIEMRKGKVSFLWIVGSGVG 2211

Qy         80 EVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSNKPKA---PAVYDLEGGSSN 136
              |    : :    ::   |::  |  :   ::       : |||   |: |
Db       2212 RVGFPDLTID----DSYWYRIEASRTGRNGSISV---RALDGPKASMVPSTYHSVSPPGY 2264

Qy        137 TLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNENVLSLYNFKTTFNLNTT 196
              |:|::|  :|: :|||     :   :|  : ||:     :  : |:||:
Db       2265 TILDVD-ANAMLFVGGLTGKIKKADAVRVITFTGCMGETYFDNKPIGLWNFRE----KEG 2319

Qy        197 EVEPCRRRKEESDKN---YFEGTGYARIPTQPNAPFPNFIQTI----QTTVDRGLLFFAE 249
              : : |    :  |      |:| ||| : ::|   :|| | |:    :|     || :
Db       2320 DCKGCTVSPQVEDSEGTIQFDGEGYALV-SRPIRWYPN-ISTVMFKFRTFSSSALLMYLA 2377

Qy        250 NQD--NFISLNIEDGNLMVRYKLNSEPPKEKGIRDTI-----NDGKDHSILITIGKLQKR 302
              :|  :|:|: : ||:: | | | |       |:   :     ||||  :   |: ::||:
Db       2378 TRDLKDFMSVELSDGHVKVSYDLGS------GMTSVVSNQNHNDGKWKA--FTLSRIQKQ 2429

Qy        303 MWINV------NERSVRIEGEIFDF-------STYYLGGIP----IAIRERFNISTPAFQ 345
              |::      | :|      :|       | ||:|    :::: |  ::   :
Db       2430 ANISIVDIDSNQEENVATSSSGNNFGLDLKADDKIYFGGLPTLRNLSMKARPEVNVKKYS 2489

Qy        346 GCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGG--QMSFTNLDVPSTDR 400
              ||:|::   :    ::   | ||||| ||   : | | || : |  :::  ::|| :
Db       2490 GCLKDIEISRTPYNILSSPDYVGVTKGCS--LENVNTVSFPKPGFVELAAVSIDVGT--- 2544

Qy        401 FQLSFGFQTFQPSGTLL------------NHQTRTSSLLVTLEDG----HIELSTRD-S 442
              :::  |  |   || :|              ||  :   : | |     |:   ||
Db       2545 -EINLSFSTRNESGIILLGSGGTLTPPRRKRRQTTQAYYAIFLNKGRLEVHLSSGTRTMR 2603

Qy        443 NIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQ-QSLRLGGG- 500
              | |   | : ||  | | |   | |:  :  |:  | | |      : : | :||
Db       2604 KIVIKPEPNLFHDGREHSVHV-ERTRGIFTVQIDEDRRHIQNLTEEQPIEVKKLFVGGAP 2662

Qy        501 ------------HFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLF 548
                         |:||: |:::         :| |      |:| : |  :  ||
Db       2663 PEFQPSPLRNIPAFQGCVWNLVINSIP-----MDFAQPIAFKNADIGRCTYQKP------ 2711

Qy        549 KSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLP-PLNTKA-------SHRAL-- 598
              | ::          ::|  ||:  :             | |: |          |  ||
Db       2712 ----REDESEAVPAEVIVQ--PQSVPT--------PAFPFPVPTMVHGPCVAESEPALLT 2757

Qy        599 ---QFGDSPTSHLLLKLPQELLKPRSQPSLDIQTTSPKGLVFYAG--TKDSFLALYVADG 653
                 ||| |  ||: :      :| |    |:::| :  ||:|| |       |  : : :|
Db       2758 GSKQFGLSRNSHIAIVFDDTKVKNRLTIELEVRTEAESGLLFYMGRINHADFGTVQLRNG 2817

Qy        654 RVVFALGAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISP 713
              |:   |    |     : :||:|| :       :  | ||   :|         ||||
Db       2818 FPFFSYDLGSGSTRTMIPTKINDGQWHKIKIVRVKQEGILYVDDASSQ--------TISP 2869

Qy        714 REQVYL---------GLPLSRKPKSL--PQHSFVGCLRDFQLNSKP--LDSPSARFGVSP 760
              ::  |          |||::  : :    :|  ||:|:  :    |  || |:: | |
Db       2870 KKADILDVGGILYVGGLPINYTTRRIGPVTYSLDGCVRNLHMEQAPVDLDQPTSSFHVGT 2929

Qy        761 CLGGSLEKGIYFSQGGGHVILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVY 820
              |   : | | ||  | |           :| :| :  |    ||||: : ||    : :
Db       2930 CFANA-ESGTYF-DGTGFGKAVGGFIVGLDLLVEFEFRTTRPTGVLLGISSQKMDGMGIE 2987

Qy        821 MEAGKVTTSVSSDAGGSVTSITPKQ---SLCDGQWHSV-AVSIKQRI 863
              |   |:   | : | |  |:|   :    :|:|||: | |   || |:
Db       2988 MIDEKLMFHVDNGA-GRFTAIYDAEIPGHMCNGQWYKVTAKKIKNRL 3033


RESULT 11
T43291
laminin alpha chain - Caenorhabditis elegans
```

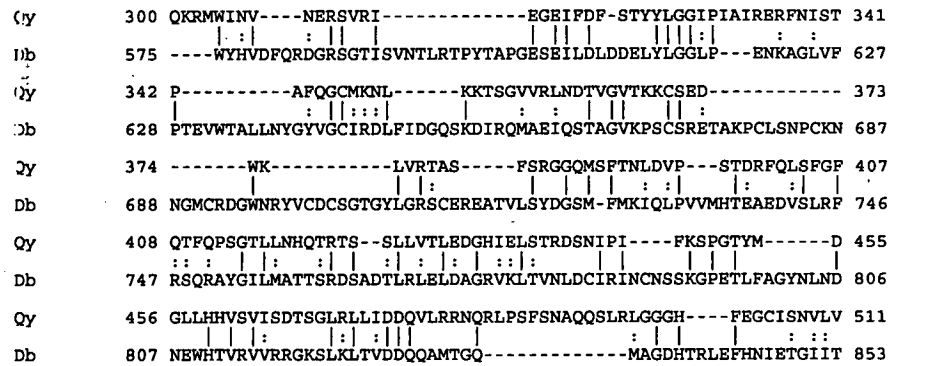
```
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43291
R;Zhu, X.; Kao, G.; Joh, K.; Hall, D.H.; Wadsworth, V.K.; Hutter, H.; Vogel, B.E.; Huang
submitted to the EMBL Data Library, June 1998
A;Description: Expression, function and evolution of laminin alpha chains.
A;Reference number: Z22397
A;Accession: T43291
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3102 <ZHU>
A;Cross-references: UNIPROT:O45614; EMBL:AF074902; PIDN:AAC26793.1
C;Genetics:
A;Map position: 1
A;Note: lama1/2
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

  Query Match             8.0%;  Score 358.5;  DB 2;  Length 3102;
  Best Local Similarity   22.1%;  Pred. No. 9.7e-16;
  Matches  185;  Conservative  154;  Mismatches  312;  Indels  187;  Gaps   44;

Qy         50 GNKDASKDYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAV--MDRVKFQRIYQ 107
Db       2308 GRRTQPSEHLAVEIRDKRVVVHWDIGSGK------KMITNSHPINYVPSNDRVTWYHIDV 2361

Qy        108 FA---KLNYT---KEATSN--KPKAPAVYDLEGGS--SNTLLNLDPEDAVFYVGGYPPDF 157
Db       2362 LRIGNAVNLTVALKESYDGGFKPRGAPVSVFVGNSKDDNSIFNTIPGETTIDVG---TDE 2418

Qy        158 ELPSRLRFPPYK-----GCIELDDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNY 212
Db       2419 TVASDIGLTTHKFSGIVGGLRIDEV---PLPLWSFEST----TGECEGATSPPKTSQRGH 2471

Qy        213 FEGTGYARIPTQPNAPFPNFIQTIQTTVD-RGLLFF--AENQDNFISLNIEDGNLMVRYK 269
Db       2472 LFRDGFANVSMSVSERTMSAITVIFNAFSPNGLLYFRGSEASGDFVAIYLNDGKVMFKIN 2531

Qy        270 LNSEPPKEKGIRDTINDGKDHSI-LITIGKLQKRMWINVNERSVR----IEGE----IFD 320
Db       2532 LGGGSVAELTSQNVYNDGKEHTVKAIRTG---SEMYLQVDSDADRFNTVITGENTALNIE 2588

Qy        321 FSTYYLGGIPIAI-RERF-NISTPAFQGCMKNLK-----------------KTSGVVRLN 361
Db       2589 NENHYVAGVPMTLNKEVFGDINWNGFIGCILTVKPSQVGELDLDHPEHSQGKTDGCSQVS 2648

Qy        362 DTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQT 421
Db       2649 ---GVTDK---------IIGFPKPGYLITKGISIDNSSTF--AFSFRTREENGTLVYQSS 2694

Qy        422 RTSSLLVTLED------GHI---------------ELSTRDSNIPIFKSPGTYMDGLLHH 460
Db       2695 KLQK--VSKRDSEDDGKGYIAFYLFRGYLVLHFGKDASSR-KEVVTFRSSHPYNDGQVHA 2751

Qy        461 VSVISDTSGLRLLIDDQVLRRNQRL---PSFSNAQQSLRLGG--------------GHF 502
Db       2752 VFMERNGKIISVKVDDKEIGDSQSLSDETSVGTTSGRLILGGFSDDLKPPNNEIPITSFF 2811

Qy        503 EGCISNVL--VQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFL-------------- 545
Db       2812 IGCISDVFLNMKRVSLAPE---------KHNAQIGMCSMDDTQGLSPIDDPIDGNGHNGH 2862

Qy        546 -----MLFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQF 600
Db       2863 RKSSKLSFEATNR-NYYEVSTQSSHLVMNPNGEETVE-----KTCETSLGSLQG--AVRY 2914

Qy        601 GDSPTSHLLLKLPQELLKPR-SQFS--LDIQTTSPKGLVF-YAGTKD--SFLALYVADGR 654
Db       2915 GLSKSSHSRINF--EAPYPNITDFTVKLSLQTETSNGMIWAWANYKNYTRYIFLDIIDGF 2972

Qy        655 VVFAL-GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISP 713
Db       2973 ATLEVKGHKQPKILKHLGNRINDGQWHDITVEKKNRSLKLIIDSLG------PVEMTDCP 3026

Qy        714 -----REQVYLGLPLSRKPK--SLPQHSFVGCLRDFQLNSK---PLDSPSARFGVSPC 761
Db       3027 TPKVMKKRVYVGGVISRHRRQFGLTTPGLDGCIRDFEMNNRIFNNLDEPSTSKNVMPC 3084


RESULT 12
I45944
neurexin I-alpha - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C;Accession: I45944
R;Ullrich, B.; Ushkaryov, Y.A.; Sudhof, T.C.
Neuron 14, 497-507, 1995
A;Title: Cartography of neurexins: more than 1000 isoforms generated by alternative spli
A;Reference number: I45944; MUID:95209856; PMID:7695896
A;Accession: I45944
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1530 <ULL>
A;Cross-references: UNIPROT:Q28146; GB:L14855; NID:g388560; PIDN:AAA74123.1; PID:g388561
C;Superfamily: neurexin; EGF homology
F;703-735/Domain: EGF homology <EGF>

  Query Match             7.2%;  Score 321.5;  DB 2;  Length 1530;
  Best Local Similarity   19.5%;  Pred. No. 1.1e-13;
  Matches  203;  Conservative  132;  Mismatches  354;  Indels  351;  Gaps   45;

Qy         35 LRENGGTEDMFVMYLGNKDASKDYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQE 94
Db       331 LQRNG-----LMLHTGK---SADYVNLALKNGAVSLVINLGSGAFEALVEPV--NGKFND 380

Qy         95 AVMDRVKFQRIYQFAKLNYTK---EATSNKPKAPAVYDLEG-----GSSNTLLNLDPEDA 146
Db       381 NAWHDVKVTR-----NLRQTSGIGHAMVNKLHCSVTISVDGILTTTGYTQEDYTMLGSDD 435

Qy        147 VFYVGGYPPDFELPSRLRFPPYKGCIELDDLNENVLSLYNFKTTFNLNTTEVEPCRRRKE 206
Db       436 FFYVGGSPSTADLPGSPVSNNFMGCLK-------------EVVYKNNDVRLELSRLAKQ 481

Qy        207 ESDKNYFEGT-------------------GYARIPTQPNAPFPNFIQTIQTTVDRGLLF 246
Db       482 GDPKMKIHGVVAFKCENVATLDPITFETPESFISLPKWNAKKTGSISFDFRTTEPNGLIL 541

Qy        247 FAENQD--------------NFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSI 292
Db       542 FSHGKPRHQKDAKHPQMIKVDFFAIEMLDGHLYLLLDMGSGTIKIKALQKKVNDGE---- 597

Qy        293 LITIGKLQKRMWINV----NERSVRI-------------EGEIFDF-STYYLGGIPIAIR 334
Db       598 -----WYHVDFQRDGRSGTISVNTLRTPYTAPGESQILDLDDELYLGGLP---E 643

Qy        335 ERFNISTP----------AFQGCMKNL------KKTSGVVRLNDTVGVTKKCSED----- 373
Db       644 NKAGLVFPTEVWTALLNYGYVGCIRDLFIDGQSKDIRQMAEVQSTAGVKPSCSRETAKPC 703

Qy        374 --------------WK-----------LVRTAS-----FSRGGQMSFTNLDVP---STDR 400
Db       704 LSNPCKNNGMCRDGWNRYVCDCSGTGYLGRSCEREATVLSYDGSM-FMKIQLPVVMHTEA 762

Qy        401 FQLSFGFQTFQPSGTLLNHQTRTS--SLLVTLEDGHIELSTRDSNIPI----FKSPGTYM 454
Db       763 EDVSLRFRSQRAYGILMATTSRDSADTLRLELDAGRVKLTVNLDCIRINCNSSKGPETLF 822

Qy        455 ------DGLLHHVSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGH----FEG 504
Db       823 AGYNLNDNEWHTVRVVRRGKSLKLTVDDQQAMTGQ------------MAGDHTRLEFHN 869

Qy        505 CISNVLVQR--FSQSPE--------------VLDLASKSTKKDASLGGCSLN-KPPFLM 546
Db       870 IETGIITERRYLSSVPSNFIGHLQSLTFNGMAYIDLC-----KNGDIDYCELNARFGFRN 924

Qy        547 LFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQFGDSPTS 606
```



RESULT 13
A40228
neurexin I-alpha precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: A40228; S27884
R;Ushkaryov, Y.A.; Petrenko, A.G.; Geppert, M.; Suedhof, T.C.
Science 257, 50-56, 1992
A;Title: Neurexins: synaptic cell surface proteins related to the alpha-latrotoxin recep
A;Reference number: A40228; MUID:92320296; PMID:1621094
A;Accession: A40228
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1507 <USH>
A;Cross-references: UNIPROT:Q63372; GB:M96374; NID:g205710; PIDN:AAA41704.1; PID:g205711
C;Superfamily: neurexin; EGF homology
C;Keywords: alternative splicing; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-1507/Product: neurexin I-alpha #status predicted <MAT>
F;680-712/Domain: EGF homology <EGF>
F;1087-1119/Domain: EGF homology <EGF1>

Query Match 7.1%; Score 320; DB 2; Length 1507;
Best Local Similarity 19.5%; Pred. No. 1.4e-13;
Matches 201; Conservative 134; Mismatches 354; Indels 344; Gaps 45;





RESULT 14
A48216
neurexin III-alpha secreted type 1 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Dec-2002
C;Accession: A48216; B48216
R;Ushkaryov, Y.A.; Suedhof, T.C.
Proc. Natl. Acad. Sci. U.S.A. 90, 6410-6414, 1993
A;Title: Neurexin IIIalpha: extensive alternative splicing generates membrane-bound and
A;Reference number: A48216; MUID:93342001; PMID:8341647
A;Accession: A48216
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1438 <USH>
A;Cross-references: GB:L14851
A;Accession: B48216
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1368,1372-1438 <US2>
A;Cross-references: GB:L14851

```
C;Genetics:
A;Introns: 1372/1
C;Superfamily: neurexin; EGF homology
C;Keywords: alternative splicing; brain; cell surface component; duplication; extracellu
F;1-27/Domain: signal sequence #status predicted <SIG>
F;202-234/Domain: EGF homology <EGF>
F;651-683/Domain: EGF homology <EGF1>

  Query Match             6.7%;  Score 301.5;  DB 2;  Length 1438;
  Best Local Similarity   19.8%;  Pred. No. 2.6e-12;
  Matches  204;  Conservative  135;  Mismatches  342;  Indels  349;  Gaps   49;

Qy         36 RENGGTEDMFVMYLGNKDASKDYIGMAVVDGQLTCVYNLGD------------------ 76
              : ||       ::: |      | ||: :|: || :: | |||
Db        295 QRNG-----LILHTGK---SADYVNLALKDGAVSLVINLGSGAFEAIVEPVNGKFNDNAW 346

Qy         77 ---------REAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSNKPKAPAV 127
                       |:  : :| :|| :                          ||:|
Db        347 HDVKVTRNLRQVTISVDGILTTT--------------------GYTQE----------- 374

Qy        128 YDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIE------------- 173
                     |:|     |  ||||| |       :||         : ||::
Db        375 -------DYTMLG---SDDFFYVGGSPSTADLPGSPVSNNFMGCLKEVVYKNNDIRLELS 424

Qy        174 -LDDLNENVLSLYN---FKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPF 229
               |  : :  : :|     ||      |      ::|          |:       |   :|
Db        425 RLARIGDTKMKIYGEVVFKCE---NVATLDPI---------NFETPEAYISLPKWNTKRM 472

Qy        230 PNFIQTIQTTVDRGLLFFA-----ENQD---------NFISLNIEDGNLMVRYKLNSEPP 275
                :       :||    ||: |         | :|           :| :: : |||| :    : |
Db        473 GSISFDFRTTEPNGLILFTHGKPQERKDVRSQKNTKVDFFAVELLDGNLYLLLDMGSGTI 532

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNERSVRI----EGEIFDF-STYYLGGIP 330
              | |  :    |||: :   : |  :    :  |:||  |            | || |     ||||:|
Db        533 KVKATQKKANDGEWYH--VDIQRDGRSGTISVNSRRTPFTASGESEILDLEGDMYLGGLP 590

Qy        331 IAIRERFNISTP----------AFQGCMKNL------KKTSGVVRLNDTVGVTKKCS--- 371
                  |    :    |           : ||:::|       |    :  :    ||   ||
Db        591 ---ENRAGLILPTELWTAMLNYGYVGCIRDLFIDGRSKNIRQLAEMQNAAGVKSSCSRMS 647

Qy        372 ----------------EDWK---------------LVRTAS-FSRGGQMSFTNLDVP--- 396
                              : |                 | ||   |   | |  :   : :|
Db        648 AKQCDSYPCKNNAVCKDGWNRFICDCTGTGYWGRTCEREASILSYDGSM-YMKVIMPMVM 706

Qy        397 STDRFQLSFGFQTFQPSGTLLNHQTRTS--SLLVTLEDGHIELSTRDSNIPI----FKSP 450
               |:   :||  | :  :   | |:    :| |   :| : |: | ::|         ||        | |
Db        707 HTEAEDVSFRFMSQRAYGLLVATTSRDSADTLRLELDGGRVKLMVNLDCIRINCNSSKGP 766

Qy        451 GTYM------DGLLHHVSVISDTSGLRLLIDDQV-----LRRNQRLPSFSNAQQSLRLGG 499
                |         | | | |:       |:| :|| |       :  : ||  | | | :  :
Db        767 ETLYAGQKLNDNEWHTVRVVRRGKSLKLTVDDDVAEGTMVGDHTRL-EFHNIETGIMTEK 825

Qy        500 -----------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLF 548
                         || : :  | |:            :||            |: :   | |
Db        826 RYISVVPSSFIGHLQSLMFNGLL--------YIDLC-----KNGDIDYCEL--------- 863

Qy        549 KSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQFGDSPTS-H 607
                      | | |  :  :: |                        ||:|:  |       : || |
Db        864 -------KAR-FGLRNIIADP-----------------VTFKTKSSYLTLATLQAYTSMH 898

Qy        608 LLLKLPQELLKPRSQFSLDIQTTSPKG-LVFYAGTKDSFLALYVADGRV--VFALGAGGK 664
              |  :                  :|||  | ::| :|  : |:|: :   |  :  || || |
Db        899 LFFQ---------------FKTTSADGFILFNSGDGNDFIAVELVKGYIHYVFDLGNGPN 943

Qy        665 KLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL-GLP- 722
               ::   |     :| :|| ||       :         :   |     :    :   :|: ||
Db        944 VIKGNSDRPLNDNQWHNVVITRDNSNTHSLKVDTKVVTQVINGAKNLDLKGDLYMAGLAQ 1003

Qy        723 --LSRKPKSL-PQHSFVGCLRDFQLNSKPLD-----------------SPSARFGVSPCL 762
                 |  ||  :  :   | |||    ||  : |                       ||      ||
Db       1004 GMYSNLPKLVASRDGFQGCLASVDLNGRLPDLINDALHRSGQIDRGCEGPSTTCQEDSC- 1062

Qy        763 GGSLEKGI-----------------------------YFSQGGGHVILANSVSLGP---- 789
                   :|:                                 | : || ::     :  |
Db       1063 ---ANQGVCMQQWEGFTCDCSMTSYSGNQCNDPGATYIFGKSGGLILYTWPANDRPSTRS 1119

Qy        790 -ELKLTFSIRPRSLTGVLIHVGSQS--GQRLSVYMEAGKVTTSVSSDAGGSVTSITPKQS 846
                | : ||   :    |:|: : |     |   | :::| ||:   |   :  |    ||  :::
Db       1120 DRLAVGFSTTVKD--GILVRIDSAPGLGDFLQLHIEQGKI--GVVFNIGTVDISIKEERT 1175

Qy        847 -LCDGQWHSV 855
                : ||::| |
Db       1176 PVNDGKYHVV 1185


RESULT 15
B48218
neurexin III-alpha membrane-bound type 3 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Dec-2002
C;Accession: B48218; C48218
R;Ushkaryov, Y.A.; Suedhof, T.C.
Proc. Natl. Acad. Sci. U.S.A. 90, 6410-6414, 1993
A;Title: Neurexin IIIalpha: extensive alternative splicing generates membrane-bound and
A;Reference number: A48216; MUID:93342001; PMID:8341647
A;Accession: B48218
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1471 <USH>
A;Cross-references: GB:L14851
A;Accession: C48218
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1368,1372-1471 <US2>
A;Cross-references: GB:L14851
C;Genetics:
A;Introns: 1372/1
C;Superfamily: neurexin; EGF homology
C;Keywords: alternative splicing; brain; cell surface component; duplication; receptor;
F;1-27/Domain: signal sequence #status predicted <SIG>
F;202-234/Domain: EGF homology <EGF>
F;651-683/Domain: EGF homology <EGF1>

  Query Match             6.7%;  Score 301.5;  DB 2;  Length 1471;
  Best Local Similarity   19.8%;  Pred. No. 2.7e-12;
  Matches  204;  Conservative  135;  Mismatches  342;  Indels  349;  Gaps   49;

Qy         36 RENGGTEDMFVMYLGNKDASKDYIGMAVVDGQLTCVYNLGD------------------ 76
              : ||       ::: |      | ||: :|: || :: | |||
Db        295 QRNG-----LILHTGK---SADYVNLALKDGAVSLVINLGSGAFEAIVEPVNGKFNDNAW 346

Qy         77 ---------REAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSNKPKAPAV 127
                       |:  : :| :|| :                          ||:|
Db        347 HDVKVTRNLRQVTISVDGILTTT--------------------GYTQE----------- 374

Qy        128 YDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIE------------- 173
                     |:|     |  ||||| |       :||         : ||::
Db        375 -------DYTMLG---SDDFFYVGGSPSTADLPGSPVSNNFMGCLKEVVYKNNDIRLELS 424

Qy        174 -LDDLNENVLSLYN---FKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPF 229
               |  : :  : :|     ||      |      ::|          |:       |   :|
Db        425 RLARIGDTKMKIYGEVVFKCE---NVATLDPI---------NFETPEAYISLPKWNTKRM 472

Qy        230 PNFIQTIQTTVDRGLLFFA-----ENQD---------NFISLNIEDGNLMVRYKLNSEPP 275
                :       :||    ||: |         | :|           :| :: : |||| :    : |
Db        473 GSISFDFRTTEPNGLILFTHGKPQERKDVRSQKNTKVDFFAVELLDGNLYLLLDMGSGTI 532

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNERSVRI----EGEIFDF-STYYLGGIP 330
              | |  :    |||: :   : |  :    :  |:||  |            | || |     ||||:|
Db        533 KVKATQKKANDGEWYH--VDIQRDGRSGTISVNSRRTPFTASGESEILDLEGDMYLGGLP 590

Qy        331 IAIRERFNISTP----------AFQGCMKNL------KKTSGVVRLNDTVGVTKKCS--- 371
                  |    :    |           : ||:::|       |    :  :    ||   ||
Db        591 ---ENRAGLILPTELWTAMLNYGYVGCIRDLFIDGRSKNIRQLAEMQNAAGVKSSCSRMS 647

Qy        372 ----------------EDWK---------------LVRTAS-FSRGGQMSFTNLDVP--- 396
```

```
Db        648 AKQCDSYPCKNNAVCKDGWNRFICDCTGTGYWGRTCEREASILSYDGSM-YMKVIMPMVM 706

Qy        397 STDRFQLSFGFQTFQPSGTLLNHQTRTS--SLLVTLEDGHIELSTRDSNIPI----FKSP 450

Db        707 HTEAEDVSFRFMSQRAYGLLVATTSRDSADTLRLELDGGRVKLMVNLDCIRINCNSSKGP 766

Qy        451 GTYM------DGLLHHVSVISDTSGLRLLIDDQV-----LRRNQRLPSFSNAQQSLRLGG 499

Db        767 ETLYAGQKLNDNEWHTVRVVRRGKSLKLTVDDDVAEGTMVGDHTRL-EFHNIETGIMTEK 825

Qy        500 -----------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLF 548

Db        826 RYISVVPSSFIGHLQSLMFNGLL--------YIDLC-----KNGDIDYCEL--------- 863

Qy        549 KSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQFGDSPTS-H 607

Db        864 -------KAR-FGLRNIIADP----------------VTFKTKSSYLTLATLQAYTSMH 898

Qy        608 LLLKLPQELLKPRSQFSLDIQTTSPKG-LVFYAGTKDSFLALYVADGRV--VPALGAGGK 664

Db        899 LFFQ--------------FKTTSADGFILFNSGDGNDFIAVELVKGYIHYVFDLGNGPN 943

Qy        665 KLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL-GLP- 722

Db        944 VIKGNSDRPLNDNQWHNVVITRDNSNTHSLKVDTKVVTQVINGAKNLDLKGDLYMAGLAQ 1003

Qy        723 --LSRKPKSL-PQHSFVGCLRDFQLNSKPLD----------------SPSARFGVSPCL 762

Db       1004 GMYSNLPKLVASRDGFQGCLASVDLNGRLPDLINDALHRSGQIDRGCEGPSTTCQEDSC- 1062

Qy        763 GGSLEKGI----------------------------YFSQGGGHVILANSVSLGP---- 789

Db       1063 ---ANQGVCMQQWEGFTCDCSMTSYSGNQCNDPGATYIFGKSGGLILYTWPANDRPSTRS 1119

Qy        790 -ELKLTFSIRPRSLTGVLIHVGSQS--GQRLSVYMEAGKVTTSVSSDAGGSVTSITPKQS 846

Db       1120 DRLAVGFSTTVKD--GILVRIDSAPGLGDFLQLHIEQGKI--GVVFNIGTVDISIKEERT 1175

Qy        847 -LCDGQWHSV 855

Db       1176 PVNDGKYHVV 1185
```

Search completed: February 22, 2005, 08:19:35
Job time : 29.1073 secs

This Page Blank (uspto)

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:07:29 ; Search time 146.522 Seconds
(without alignments)
3026.590 Million cell updates/sec

Title: US-10-817-423-2
Perfect score: 4491
Sequence: 1 MRFNGKSGVEVRLPNDLEDL.....LCDGQWHSVAVSIKQRILHL 866

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4491	100.0	1725	2	P70570	P70570 rattus norv
2	4043	90.0	3333	1	LMA3_MOUSE	Q61789 mus musculu
3	3562.5	79.3	1668	2	Q6VU69	Q6vu69 homo sapien
4	3562.5	79.3	3277	2	Q6VU67	Q6vu67 homo sapien
5	3562.5	79.3	3333	2	Q6VU68	Q6vu68 homo sapien
6	3560.5	79.3	1713	1	LMA3_HUMAN	Q16787 homo sapien
7	3560.5	79.3	1806	2	Q96TG0	Q96tg0 homo sapien
8	3560.5	79.3	3333	2	Q76E14	Q76e14 homo sapien
9	3331	74.2	1725	2	Q867A1	Q867a1 canis famil
10	1190	26.5	1816	1	LMA4_HUMAN	Q16363 homo sapien
11	1185	26.4	1254	2	Q91VV0	Q91vv0 mus musculu
12	1185	26.4	1816	1	LMA4_MOUSE	P97927 mus musculu
13	1042.5	23.2	3695	1	LMA5_HUMAN	O15230 homo sapien
14	1042.5	23.2	3695	2	Q8TDF8	Q8tdf8 homo sapien
15	950	21.2	1524	2	Q6ZQA1	Q6zqa1 mus musculu
16	948	21.1	3718	1	LMA5_MOUSE	Q61001 mus musculu
17	636.5	14.2	3712	1	LMA_DROME	Q00174 drosophila
18	636.5	14.2	3712	2	Q9VRW0	Q9vrw0 drosophila
19	629	14.0	3616	2	Q7PPF9	Q7ppf9 anopheles g
20	625	13.9	670	2	Q9BTT3	Q9btt3 homo sapien
21	600.5	13.4	3672	1	LML2_CAEEL	Q21313 caenorhabdi
22	594	13.2	794	2	Q8R3Y7	Q8r3y7 mus musculu
23	579.5	12.9	1518	2	Q21442	Q21442 caenorhabdi
24	579.5	12.9	3704	2	P91904	P91904 caenorhabdi
25	545	12.1	3084	1	LMA1_MOUSE	P19137 mus musculu
26	529.5	11.8	3075	1	LMA1_HUMAN	P25391 homo sapien
27	526.5	11.7	3110	1	LMA2_HUMAN	P24043 homo sapien
28	523.5	11.7	414	2	Q14731	Q14731 homo sapien
29	516.5	11.5	3106	1	LMA2_MOUSE	Q60675 mus musculu
30	514	11.4	354	2	Q91YG8	Q91yg8 mus musculu
31	510	11.4	858	2	Q8R145	Q8r145 mus musculu
32	442	9.8	3375	2	Q8IP51	Q8ip51 drosophila
33	425	9.5	3367	2	Q9XZC9	Q9xzc9 drosophila
34	422.5	9.4	747	2	Q7Z5W6	Q7z5w6 homo sapien
35	398	8.9	659	2	Q7TQI9	Q7tqi9 mus musculu
36	374	8.3	3170	2	Q7PN80	Q7pn80 anopheles g
37	358.5	8.0	3102	2	O45614	O45614 caenorhabdi
38	335	7.5	559	2	Q6P6D3	Q6p6d3 homo sapien
39	332.5	7.4	1363	1	NX1A_CHICK	Q9ddd0 gallus gall
40	325.5	7.2	1514	1	NX1A_RAT	Q63372 rattus norv
41	322	7.2	1553	2	Q8CHE6	Q8che6 mus musculu
42	321.5	7.2	1530	1	NX1A_BOVIN	Q28146 bos taurus
43	320	7.1	1176	2	Q80Y87	Q80y87 mus musculu
44	318	7.1	1477	1	NX1A_HUMAN	Q9ulb1 homo sapien
45	316	7.0	1392	2	Q8IUE3	Q8iue3 homo sapien

ALIGNMENTS

RESULT 1
P70570
ID P70570 PRELIMINARY; PRT; 1725 AA.
AC P70570;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Laminin-5 alpha 3 chain.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97081969; PubMed=8923212;
RA Baker S.E., Hopkinson S.B., Fitchmun M., Andreason G.L., Frasier F.,
RA Plopper G., Quaranta V., Jones J.C.R.;
RT "Laminin-5 and hemidesmosomes: role of the alpha 3 chain subunit in
RT hemidesmosome stability and assembly.";
RL J. Cell Sci. 109:2509-2520(1996).
DR EMBL; U61261; AAB17053.1; -.
DR HSSP; P35070; 1IP0.
DR GO; GO:0005606; C:laminin-1; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR GO; GO:0030334; P:regulation of cell migration; IEA.
DR GO; GO:0045995; P:regulation of embryonic development; IEA.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00053; Laminin_EGF; 2.
DR Pfam; PF02210; Laminin_G_2; 4.
DR Pfam; PF06008; Laminin_I; 1.
DR Pfam; PF06009; Laminin_II; 1.
DR SMART; SM00180; EGF_Lam; 2.
DR SMART; SM00282; LamG; 5.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW Laminin EGF-like domain.
SQ SEQUENCE 1725 AA; 190392 MW; 02EE43B33E72B0FB CRC64;

Query Match 100.0%; Score 4491; DB 2; Length 1725;
Best Local Similarity 100.0%; Pred. No. 5e-293;
Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db        782 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 841

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 901

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 961

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 1021

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 1081

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 1141

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 1201

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 1261

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 1321

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQF 1381

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALG 1441

Qy        661 AGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYLG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 AGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYLG 1501

Qy        721 LPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1502 LPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHVI 1561

Qy        781 LANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTS 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 LANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTS 1621

Qy        841 ITPKQSLCDGQWHSVAVSIKQRILHL 866
              ||||||||||||||||||||||||||
Db       1622 ITPKQSLCDGQWHSVAVSIKQRILHL 1647


RESULT 2
LMA3_MOUSE
ID   LMA3_MOUSE     STANDARD;      PRT;  3333 AA.
AC   Q61789; O08751; Q61788; Q61966; Q9JHQ7;
DT   01-NOV-1997 (Rel. 35, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Laminin alpha-3 chain precursor (Nicein alpha subunit).
GN   Name=Lama3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE OF 1-58 FROM N.A., AND SEQUENCE OF 32-38.
RX   MEDLINE=21818471; PubMed=11829758; DOI=10.1042/0264-6021:3620213;
RA   Garbe J.H., Gohring W., Mann K., Timpl R., Sasaki T.;
RT   "Complete sequence, recombinant analysis and binding to laminins and
RT   sulphated ligands of the N-terminal domains of laminin alpha3B and
RT   alpha5 chains.";
RL   Biochem. J. 362:213-221(2002).
RN   [2]
RP   SEQUENCE OF 1-726 FROM N.A.
RC   STRAIN=ICR;
RX   MEDLINE=97296337; PubMed=9151674; DOI=10.1083/jcb.137.3.685;
RA   Miner J.H., Patton B.L., Lentz S.I., Gilbert D.J., Snider W.D.,
RA   Jenkins N.A., Copeland N.G., Sanes J.R.;
RT   "The laminin alpha chains: expression, developmental transitions, and
RT   chromosomal locations of alpha1-5, identification of heterotrimeric
RT   laminins 8-11, and cloning of a novel alpha3 isoform.";
RL   J. Cell Biol. 137:685-701(1997).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM A), AND SEQUENCE OF 716-3284 FROM N.A.
RP   (ISOFORM B).
RC   STRAIN=BALB/c; TISSUE=Lung;
RX   MEDLINE=95394948; PubMed=7665604; DOI=10.1074/jbc.270.37.21820;
RA   Galliano M.-F., Aberdam D., Aguzzi A., Ortonne J.-P., Meneguzzi G.;
RT   "Cloning and complete primary structure of the mouse laminin alpha 3
RT   chain. Distinct expression pattern of the laminin alpha 3A and alpha
RT   3B chain isoforms.";
RL   J. Biol. Chem. 270:21820-21826(1995).
RN   [4]
RP   REVISIONS.
RA   Aberdam D.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 1767-2485 FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=94281750; PubMed=8012114;
RA   Aberdam D., Galliano M.-F., Mattei M.-G., Pisani-Spadafora A.,
RA   Ortonne J.-P., Meneguzzi G.;
RT   "Assignment of mouse nicein genes to chromosomes 1 and 18.";
RL   Mamm. Genome 5:229-233(1994).
RN   [6]
RP   SEQUENCE OF 1767-2485 FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=94363405; PubMed=8081888;
RA   Aberdam D., Aguzzi A., Baudoin C., Galliano M.-F., Ortonne J.-P.,
RA   Meneguzzi G.;
RT   "Developmental expression of nicein adhesion protein (laminin-5)
RT   subunits suggests multiple morphogenic roles.";
RL   Cell Adhes. Commun. 2:115-129(1994).
CC   -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC       is thought to mediate the attachment, migration and organization
CC       of cells into tissues during embryonic development by interacting
CC       with other extracellular matrix components.
CC   -!- FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
CC       via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-
CC       6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine
CC       phosphorylation of pp125-FAK and p80, (3) differentiation of
CC       keratinocytes (By similarity).
CC   -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC       different polypeptide chains (alpha, beta, gamma), which are bound
CC       to each other by disulfide bonds into a cross-shaped molecule
CC       comprising one long and three short arms with globules at each
CC       end. The alpha-3 chain is a subunit of laminin-5
CC       (epiligrin/kalinin/nicein), and possibly also a component of
CC       laminin-6 (K-laminin) and laminin-7 (KS-laminin).
CC   -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC       membranes (major component).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=B;
CC         IsoId=Q61789-1; Sequence=Displayed;
CC       Name=A;
CC         IsoId=Q61789-2; Sequence=VSP_003038, VSP_003039;
CC   -!- TISSUE SPECIFICITY: Basal membrane of the upper alimentary tract
```

```
CC       and urinary and nasal epithelia, salivary glands and teeth (both
CC       variants). Isoform A is predominantly expressed in skin, hair
CC       follicles and developing neurons of the trigeminal ganglion.
CC       Isoform B was found in bronchi, alveoli, stomach, intestinal
CC       crypts, whisker pads, CNS, telencephalic neuroectoderm, thalamus,
CC       Rathke's pouch and periventricular subependymal germinal layer.
CC   -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC       with other laminin chains to form a coiled coil structure.
CC   -!- DOMAIN: Domains IV and G are globular.
CC   -!- SIMILARITY: Contains 15 laminin EGF-like domains.
CC   -!- SIMILARITY: Contains 5 laminin G-like domains.
CC   -!- SIMILARITY: Contains 1 laminin IV domain.
CC   -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ293592; CAB99254.2; -.
DR   EMBL; U88353; AAC53179.1; -.
DR   EMBL; X84014; CAA58837.1; -.
DR   EMBL; X84013; CAA58836.1; ALT_FRAME.
DR   EMBL; L20478; AAA68091.1; -.
DR   HSSP; P02468; 1NPE.
DR   MGD; MGI:99909; Lama3.
DR   GO; GO:0005604; C:basement membrane; IDA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR008212; Lam_N2.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR008211; Laminin_N.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 10.
DR   Pfam; PF00054; Laminin_G; 3.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   Pfam; PF00055; Laminin_N; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   ProDom; PD003031; Laminin_B; 1.
DR   PROSITE; PS00022; EGF_1; 10.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 10.
KW   Alternative splicing; Basement membrane; Cell adhesion; Coiled coil;
KW   Direct protein sequencing; Extracellular matrix; Glycoprotein;
KW   Laminin EGF-like domain; Repeat; Signal.
FT   SIGNAL       1     31
FT   CHAIN       32   3333       Laminin alpha-3 chain.
FT   DOMAIN      32    294       Laminin N-terminal (domain VI).
FT   DOMAIN     295    725       Domain V.
FT   DOMAIN     296    350       Laminin EGF-like 1.
FT   DOMAIN     353    420       Laminin EGF-like 2.
FT   DOMAIN     423    464       Laminin EGF-like 3.
FT   DOMAIN     488    530       Laminin EGF-like 4.
FT   DOMAIN     533    576       Laminin EGF-like 5.
FT   DOMAIN     582    625       Laminin EGF-like 6.
FT   DOMAIN     628    678       Laminin EGF-like 7.
FT   DOMAIN     681    725       Laminin EGF-like 8.
FT   DOMAIN     793   1262       Laminin domain IV 1 (domain IV B).
FT   DOMAIN    1263   1464       Domain III B.
FT   DOMAIN    1310   1353       Laminin EGF-like 9.
FT   DOMAIN    1354   1403       Laminin EGF-like 10.
FT   DOMAIN    1404   1454       Laminin EGF-like 11.
FT   DOMAIN    1455   1464       Laminin EGF-like 12 (N-terminal).
FT   DOMAIN    1465   1653       Laminin domain IV (domain IV A).
FT   DOMAIN    1654   1821       Domain III A.
FT   DOMAIN    1654   1686       Laminin EGF-like 12 (C-terminal).
FT   DOMAIN    1687   1733       Laminin EGF-like 13.
FT   DOMAIN    1734   1786       Laminin EGF-like 14.
FT   DOMAIN    1787   1821       Laminin EGF-like 15 (incomplete).
FT   DOMAIN    1822   2388       Domain II and I.
FT   DOMAIN    2389   2590       Laminin G-like 1.
FT   DOMAIN    2597   2759       Laminin G-like 2.
FT   DOMAIN    2766   2926       Laminin G-like 3.
FT   DOMAIN    2986   3150       Laminin G-like 4.
FT   DOMAIN    3157   3330       Laminin G-like 5.
FT   DOMAIN    1854   1983       Coiled coil (Potential).
FT   DOMAIN    2015   2060       Coiled coil (Potential).
FT   DOMAIN    2091   2168       Coiled coil (Potential).
FT   DOMAIN    2214   2241       Coiled coil (Potential).
FT   DOMAIN    2321   2386       Coiled coil (Potential).
FT   SITE      2277   2279       Cell attachment site (Potential).
FT   DISULFID  1310   1317       By similarity.
FT   DISULFID  1312   1324       By similarity.
FT   DISULFID  1326   1335       By similarity.
FT   DISULFID  1338   1351       By similarity.
FT   DISULFID  1354   1369       By similarity.
FT   DISULFID  1356   1376       By similarity.
FT   DISULFID  1378   1387       By similarity.
FT   DISULFID  1390   1401       By similarity.
FT   DISULFID  1404   1416       By similarity.
FT   DISULFID  1406   1423       By similarity.
FT   DISULFID  1425   1434       By similarity.
FT   DISULFID  1437   1452       By similarity.
FT   DISULFID  1687   1696       By similarity.
FT   DISULFID  1689   1703       By similarity.
FT   DISULFID  1706   1715       By similarity.
FT   DISULFID  1718   1731       By similarity.
FT   DISULFID  1734   1746       By similarity.
FT   DISULFID  1736   1755       By similarity.
FT   DISULFID  1757   1766       By similarity.
FT   DISULFID  1769   1784       By similarity.
FT   DISULFID  1822   1822       Interchain (Probable).
FT   DISULFID  1825   1825       Interchain (Probable).

  Query Match          90.0%;  Score 4043;  DB 1;  Length 3333;
  Best Local Similarity  89.6%;  Pred. No. 2e-262;
  Matches  776;  Conservative   38;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2390 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 2449

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              |||||||||||||| |||||||||||||||||||| ||||||||||||||||
Db       2450 MAVVDGQLTCVYNLGDGEAEVQIDQVLTESESQEAVMDRVKSQRIYQFAKLNYTKEATST 2509

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||||| |||:|  ||||||||||:|||||||||| |||| ||||||||||||||||||||
Db       2510 KPKAPGVYDMESASSNTLLNLDPENAVFYVGGYPPGFELPRRLRFPPYKGCIELDDLNEN 2569

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||     ||||||
Db       2570 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPKLSWTIQTTV 2629

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||||||||||||||:|||||||||||||||:|:|| |||:||| |
Db       2630 DRGLLFFAENQDNFISLNIEDGNLMVKYKLNSEPPKEKGIRDTINNGRDHMILISIGKSQ 2689

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              ||| ||:|: |: |||||||||||||||||||||| :||||||||||||||||||||||
Db       2690 KRMLINMNKHSIIIEGEIFDFSTYYLGGIPIAIRERFPLSTPAFQGCMKNLKKTSGVVRL 2749

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
```

```
Db       2750 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSLDRFQLSFGFQTFQPSGTLLNHQ 2809

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              |||||||||||||||| ||||||: |||||||||||||||||||||||||||||||||||
Db       2810 TRTSSLLVTLEDGHIALSTRDSSSPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 2869

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ||||| |||||||||  :|||:|||||||| ||| ||||||||:||||||:|| |||||||
Db       2870 RNQRLASFSNAQQSLSMGGGYFEGCISNVFVQRMSQSPEVLDMASKSTKRDAFLGGCSLN 2929

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQF 600
              |||||||||||| ||| | ||||||:|||||| || |||||||:|||||||||:||||||
Db       2930 KPPFLMLFKSPKGFNKARSFNVNQLLQDAPQAARSIEAWQDGKSCLPPLNTKATHRALQF 2989

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALG 660
              ||||||||| |||||||||| |||||||||| :|||: ||:|||:|||:::| |:|||| 
Db       2990 GDSPTSHLLFKLPQELLKPRLQFSLDIQTTSSRGLVFHTGTRDSFVALYLSEGHVIFALG 3049

Qy        661 AGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYLG 720
              |||||||||||||||||||:|||||:| |  |||||||||||||||||||||||||||||
Db       3050 AGGKKLRLRSKERYHDGKWHSVVFGLSGRKVHLVVDGLRAQEGSLPGNSTISPREQVYLG 3109

Qy        721 LPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHVI 780
              |  ||| |||||||||||||:|||:|||||||||| ||||||||||||||||||||||:
Db       3110 LSPSRKSKSLPQHSFVGCLRNFQLDSKPLDSPSARSGVSPCLGGSLEKGIYFSQGGGHVV 3169

Qy        781 LANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTS 840
              ||||||| | | || |||||||||||||: |||| ||||||||||::|:|||:|||
Db       3170 LANSVSLEPALTLTLSIRPRSLTGVLIHIASQSGEHLSVYMEAGKVTTSMNSEAGGTVTS 3229

Qy        841 ITPKQSLCDGQWHSVAVSIKQRILHL 866
              ||||:|||||||||| |||||  |||
Db       3230 ITPKRSLCDGQWHSVTVSIKQHTLHL 3255


RESULT 3
Q6VU69
ID   Q6VU69      PRELIMINARY;      PRT;  1668 AA.
AC   Q6VU69;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Laminin alpha 3 splice variant a.
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
RA   McLean W.H., Irvine A.D., Hamill K.J., Whittock N.V.,
RA   Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
RA   Dopping-Hepenstal P.J., Eady R.A., Jamil T., Phillips R.J.,
RA   Shabbir S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
RA   Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
RA   McGrath J.A.;
RT   "An unusual N-terminal deletion of the laminin {alpha}3a isoform leads
RT   to the chronic granulation tissue disorder laryngo-onycho-cutaneous
RT   syndrome.";
RL   Hum. Mol. Genet. 12:2395-2409(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   McLean W.H.I.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY327114; AAQ72569.1; -.
DR   GO; GO:0005606; C:laminin-1; IEA.
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00053; Laminin_EGF; 1.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   SMART; SM00180; EGF_Lam; 2.
DR   SMART; SM00282; LamG; 5.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Laminin EGF-like domain.
SQ   SEQUENCE   1668 AA;  184053 MW;  9EBF5FC45637645C CRC64;

  Query Match             79.3%;  Score 3562.5;  DB 2;  Length 1668;
  Best Local Similarity   78.4%;  Pred. No. 1.6e-230;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||: |||||||:|||||||||||:||||
Db        726 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 785

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              |||||||||||||||||||:|:||:|:||::|||||||||||||||:|||| |||:
Db        786 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 845

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: |||||||||||:||||| ||||||||||||||||
Db        846 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 905

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| |||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        906 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 965

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||| |||:|: | ||:|:|||| | ||||| 
Db        966 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1025

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||||:|||||||||||||||
Db       1026 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1085

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:|||||||:|||:| :| ||  | |||||||||| ||:||
Db       1086 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1145

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||:||
Db       1146 TWTRNLQVTLEDGYIELSTSDSGSPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1205

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ::||   |:::||||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1206 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1265

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1266 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1323

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| ||||||||||||::|:|||| :|||: |||:||:|||:: ||:||||
Db       1324 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1383

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       1384 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 1443
```

```
Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :||||||::|||:|||| :||: |||| |||| |||||||: ||||
Db       1444 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1503

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || |||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1504 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1563

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:||||||||||||||||:||| ||||
Db       1564 SVTPKQSLCDGQWHSVAVTIKQHILHL 1590


RESULT 4
Q6VU67
ID   Q6VU67      PRELIMINARY;      PRT;  3277 AA.
AC   Q6VU67;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Laminin alpha 3 splice variant b2.
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
RA   McLean W.H., Irvine A.D., Hamill K.J., Whittock N.V.,
RA   Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
RA   Dopping-Hepenstal P.J., Eady R.A., Jamil T., Phillips R.J.,
RA   Shabbir S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
RA   Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
RA   McGrath J.A.;
RT   "An unusual N-terminal deletion of the laminin {alpha}3a isoform leads
RT   to the chronic granulation tissue disorder laryngo-onycho-cutaneous
RT   syndrome.";
RL   Hum. Mol. Genet. 12:2395-2409(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   McLean W.H.I.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY327116; AAQ72571.1; -.
DR   GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR   GO; GO:0005606; C:laminin-1; IEA.
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR008211; Laminin_N.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 8.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   Pfam; PF00055; Laminin_N; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   ProDom; PD003031; Laminin_B; 1.
DR   SMART; SM00181; EGF; 8.
DR   SMART; SM00180; EGF_Lam; 14.
DR   SMART; SM00281; LamB; 1.
DR   SMART; SM00282; LamG; 5.
DR   SMART; SM00136; LamNT; 1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; 12.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 13.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Laminin EGF-like domain.
SQ   SEQUENCE   3277 AA;  360209 MW;  3ACFFE998357122E CRC64;

  Query Match             79.3%;  Score 3562.5;  DB 2;  Length 3277;
  Best Local Similarity   78.4%;  Pred. No. 4.6e-230;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||||||: |||||||:||||||||||:||||
Db       2335 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 2394

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db       2395 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 2454

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :||||||||||: |||||||||||:|||| |||||||||||||||
Db       2455 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 2514

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| |||||||||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db       2515 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 2574

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||| |||:|: | ||:|:|||| | |||||
Db       2575 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 2634

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||||||:|||||||||||||||
Db       2635 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 2694

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       2695 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 2754

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| |||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       2755 TWTRNLQVTLEDGYIELSTSDSGSPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 2814

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       2815 NSKRLKHISSSRQSLRLGGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 2874

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       2875 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 2932

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| ||||||||||||::|:|||| :|||: |||:||:|||:: ||:||||
Db       2933 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 2992

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||||| |  |||
Db       2993 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRARERGSLPGNSTISIRAPVYL 3052

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :||||||::|||:|||| :||: |||| |||| |||||||: ||||
Db       3053 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 3112

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || |||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       3113 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 3172

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:||||||||||||||||:||| ||||
```

```
Db       3173 SVTPKQSLCDGQWHSVAVTIKQHILHL 3199


RESULT 5
Q6VU68
ID   Q6VU68      PRELIMINARY;      PRT;  3333 AA.
AC   Q6VU68;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Laminin alpha 3 splice variant b1.
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
RA   McLean W.H., Irvine A.D., Hamill K.J., Whittock N.V.,
RA   Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
RA   Dopping-Hepenstal P.J., Eady R.A., Jamil T., Phillips R.J.,
RA   Shabbir S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
RA   Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
RA   McGrath J.A.;
RT   "An unusual N-terminal deletion of the laminin {alpha}3a isoform leads
RT   to the chronic granulation tissue disorder laryngo-onycho-cutaneous
RT   syndrome.";
RL   Hum. Mol. Genet. 12:2395-2409(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   McLean W.H.I.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY327115; AAQ72570.1; -.
DR   GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR   GO; GO:0005606; C:laminin-1; IEA.
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR008211; Laminin_N.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 8.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   Pfam; PF00055; Laminin_N; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   ProDom; PD003031; Laminin_B; 1.
DR   SMART; SM00181; EGF; 8.
DR   SMART; SM00180; EGF_Lam; 14.
DR   SMART; SM00281; LamB; 1.
DR   SMART; SM00282; LamG; 5.
DR   SMART; SM00136; LamNT; 1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; 12.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 13.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Laminin EGF-like domain.
SQ   SEQUENCE   3333 AA;  366646 MW;  9F99AF49B8EF27DD CRC64;
```

```
  Query Match             79.3%;  Score 3562.5;  DB 2;  Length 3333;
  Best Local Similarity   78.4%;  Pred. No. 4.7e-230;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||: ||||||:|||||||||||:||||
Db       2391 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 2450

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db       2451 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 2510

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| |||||||||||||||||
Db       2511 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 2570

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||:||||:|| | | |||||||
Db       2571 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 2630

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       2631 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 2690

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||:|||||||||||||||
Db       2691 KRMWINVDVQNTIIDGEVFDPSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 2750

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       2751 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 2810

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| |||||:||||| ||  |||||| |||||||:|||||| ||||||||||:||
Db       2811 TWTRNLQVTLEDGYIELSTSDSGSPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 2870

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       2871 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 2930

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       2931 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 2988

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| |||||||||||::|:|||| :|||: |||:||:|||:: ||:||||
Db       2989 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 3048

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       3049 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 3108

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :|||||::|||:|||| :||: |||| |||| ||||||||: ||||
Db       3109 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 3168

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || ||||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       3169 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 3228

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:|||||||||||||:||| ||||
Db       3229 SVTPKQSLCDGQWHSVAVTIKQHILHL 3255


RESULT 6
LMA3_HUMAN
ID   LMA3_HUMAN      STANDARD;      PRT;  1713 AA.
AC   Q16787; Q13679; Q13680;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
```

```
DE   Laminin alpha-3 chain precursor (Epiligrin 170 kDa subunit) (E170)
DE   (Nicein alpha subunit).
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Keratinocytes;
RX   MEDLINE=94357926; PubMed=8077230;
RA   Ryan M.C., Tizard R., Vandevanter D.R., Carter W.G.;
RT   "Cloning of the LamA3 gene encoding the alpha 3 chain of the adhesive
RT   ligand epiligrin. Expression in wound repair.";
RL   J. Biol. Chem. 269:22779-22787(1994).
RN   [2]
RP   SEQUENCE OF 1-1331 FROM N.A. (ISOFORMS A AND B).
RX   MEDLINE=96163880; PubMed=8586427;
RA   Vidal F., Baudoin C., Miquel C., Galliano M.-F., Christiano A.M.,
RA   Uitto J., Ortonne J.-P., Meneguzzi G.;
RT   "Cloning of the laminin alpha 3 chain gene (LAMA3) and identification
RT   of a homozygous deletion in a patient with Herlitz junctional
RT   epidermolysis bullosa.";
RL   Genomics 30:273-280(1995).
RN   [3]
RP   DISEASE.
RX   PubMed=12915477; DOI=10.1093/hmg/ddg234;
RA   Irwin McLean W.H., Irvine A.D., Hamill K.J., Whittock N.V.,
RA   Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
RA   Dopping-Hepenstal P.J.H., Eady R.A.J., Jamil T., Phillips R.J.,
RA   Shabbir S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
RA   Darling J., Atherton D.J., Van Steensel M.A.M., Munro C.S.,
RA   Smith F.J.D., McGrath J.A.;
RT   "An unusual N-terminal deletion of the laminin alpha3a isoform leads
RT   to the chronic granulation tissue disorder laryngo-onycho-cutaneous
RT   syndrome.";
RL   Hum. Mol. Genet. 12:2395-2409(2003).
CC   -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC       is thought to mediate the attachment, migration and organization
CC       of cells into tissues during embryonic development by interacting
CC       with other extracellular matrix components.
CC   -!- FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
CC       via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-
CC       6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine
CC       phosphorylation of pp125-FAK and p80, (3) differentiation of
CC       keratinocytes.
CC   -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC       different polypeptide chains (alpha, beta, gamma), which are bound
CC       to each other by disulfide bonds into a cross-shaped molecule
CC       comprising one long and three short arms with globules at each
CC       end. The alpha-3 chain is a subunit of laminin-5
CC       (epiligrin/kalinin/nicein), and possibly also a component of
CC       laminin-6 (K-laminin) and laminin-7 (KS-laminin).
CC   -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC       membranes (major component).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=A;
CC         IsoId=Q16787-1; Sequence=Displayed;
CC       Name=B;
CC         IsoId=Q16787-2; Sequence=VSP_003037;
CC         Note=Incomplete sequence;
CC   -!- TISSUE SPECIFICITY: Skin; respiratory, urinary, and digestive
CC       epithelia and in other specialized tissues with prominent
CC       secretory or protective functions. Epithelial basement membrane,
CC       and epithelial cell tongue that migrates into a wound bed. A
CC       differential and focal expression of the alpha-3 chain is observed
CC       in the CNS.
CC   -!- INDUCTION: Laminin-5 is up-regulated in wound sites of human skin.
CC   -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC       with other laminin chains to form a coiled coil structure.
CC   -!- DOMAIN: Domain G is globular.
CC   -!- DISEASE: Defects in LAMA3 are a cause of junctional epidermolysis
CC       bullosa gravis (JEB) [MIM:226700]; also known as junctional
CC       epidermolysis bullosa Herlitz-Pearson type. JEB is a blistering
CC       disorder in skin that is characterized by a separation of basal
CC       cells from the basement membrane due to a decreased number of
CC       hemidesmosomes. Laminin-5 is missing from the basement membrane of
CC       patients with the gravis form of epidermolysis bullosa.
CC   -!- DISEASE: Defects in LAMA3 are the cause of laryngoonychocutaneous
CC       syndrome (LOCS) [MIM:245660]. LOCS is an autosomal recessive
CC       epithelial disorder confined to the Punjabi Muslim population. The
CC       condition is characterized by cutaneous erosions, nail dystrophy
CC       and exuberant vascular granulation tissue in certain epithelia,
CC       especially conjunctiva and larynx.
CC   -!- SIMILARITY: Contains 3 laminin EGF-like domains.
CC   -!- SIMILARITY: Contains 5 laminin G-like domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L34155; AAA59483.1; -.
DR   EMBL; X85107; CAA59428.1; -.
DR   EMBL; X85108; CAA59429.1; -.
DR   PIR; A55347; A55347.
DR   HSSP; P02468; 1NPE.
DR   Genew; HGNC:6483; LAMA3.
DR   MIM; 600805; -.
DR   MIM; 226700; -.
DR   MIM; 245660; -.
DR   GO; GO:0005604; C:basement membrane; TAS.
DR   GO; GO:0008544; P:epidermal differentiation; TAS.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00053; Laminin_EGF; 2.
DR   Pfam; PF00054; Laminin_G; 2.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Alternative splicing; Basement membrane; Cell adhesion; Coiled coil;
KW   Epidermolysis bullosa; Extracellular matrix; Glycoprotein;
KW   Laminin EGF-like domain; Repeat; Signal.
FT   SIGNAL       1     20       Potential.
FT   CHAIN       21   1713       Laminin alpha-3 chain.
FT   DOMAIN      46    201       Domain III A.
FT   DOMAIN      67    113       Laminin EGF-like 1.
FT   DOMAIN     114    166       Laminin EGF-like 2.
FT   DOMAIN     167    185       Laminin EGF-like 3 (incomplete).
FT   DOMAIN     186    769       Domain II and I.
FT   DOMAIN     770    971       Laminin G-like 1.
FT   DOMAIN     978   1140       Laminin G-like 2.
FT   DOMAIN    1147   1307       Laminin G-like 3.
FT   DOMAIN    1366   1530       Laminin G-like 4.
FT   DOMAIN    1537   1710       Laminin G-like 5.
FT   DOMAIN     231    327       Coiled coil (Potential).
FT   DOMAIN     396    548       Coiled coil (Potential).
FT   DOMAIN     594    621       Coiled coil (Potential).
FT   DOMAIN     702    765       Coiled coil (Potential).
FT   DOMAIN    1686   1713       Coiled coil (Potential).
FT   DISULFID    67     76       By similarity.
FT   DISULFID    69     83       By similarity.
FT   DISULFID    86     95       By similarity.
```

```
FT   DISULFID     98    111       By similarity.
FT   DISULFID    114    126       By similarity.
FT   DISULFID    116    135       By similarity.
FT   DISULFID    137    146       By similarity.
FT   DISULFID    149    164       By similarity.
FT   DISULFID    202    202       Interchain (Probable).
FT   DISULFID    205    205       Interchain (Probable).
FT   SITE        658    660       Cell attachment site (Potential).
FT   CARBOHYD    542    542       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    645    645       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    745    745       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    882    882       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    964    964       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1108   1108       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1131   1131       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1325   1325       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1477   1477       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1667   1667       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC      1     45       MGWLWIFGAALGQCLGYSSQQQRVPFLQPPGQSQLQASYVE
FT                                FRPS -> KVSSYGGYLTYQAKSFALPGDMVLLEKKPDVQL
FT                                TGQHMSIIYEETNTPRPDRLHHGRVHVVEGNFRHASSRAPV
FT                                SREELMTVLSRLADVRIQGLYFTETQRLTLSEVGLEEASDT
FT                                GSGRIALAVEICACPPAYAGDSC (in isoform B).
FT                                /FTId=VSP_003037.
FT   CONFLICT      5      5       W -> R (in Ref. 2).
FT   CONFLICT    123    125       ATG -> GMC (in Ref. 2).
FT   CONFLICT    481    481       M -> K (in Ref. 2).
FT   CONFLICT    754    754       R -> L (in Ref. 2).
FT   CONFLICT    969    969       E -> Q (in Ref. 2).
FT   CONFLICT   1052   1052       D -> A (in Ref. 2).
FT   CONFLICT   1184   1184       G -> A (in Ref. 2).
SQ   SEQUENCE   1713 AA;  189304 MW;  45EA9BE1017B60D3 CRC64;

  Query Match             79.3%;  Score 3560.5;  DB 1;  Length 1713;
  Best Local Similarity   78.4%;  Pred. No. 2.3e-230;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::||||||||||||||:|||||  |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||||:|||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| |||||:||||| ||  |||||| |||||||:|||||| |||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::||||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1368

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| ||||||||||||::|:|||| :||||: |||:||:|||:: ||:||||
Db       1369 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1428

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       1429 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 1488

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :|||||::|||:|||| :||: |||| |||| |||||||: ||||
Db       1489 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1548

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || ||||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1549 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1608

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:|||||||||||||:||| ||||
Db       1609 SVTPKQSLCDGQWHSVAVTIKQHILHL 1635


RESULT 7
Q96TG0
ID   Q96TG0      PRELIMINARY;      PRT;  1806 AA.
AC   Q96TG0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Alpha 3B chain of laminin-5 (Fragment).
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Aberdam D., Vidal, Baudoin, Miquel, Ortonne, Meneguzzi;
RL   Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X84900; CAA59325.1; -.
DR   HSSP; P02468; 1NPE.
DR   GO; GO:0005606; C:laminin-1; IEA.
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 2.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   ProDom; PD003031; Laminin_B; 1.
DR   SMART; SM00180; EGF_Lam; 2.
DR   SMART; SM00281; LamB; 1.
DR   SMART; SM00282; LamG; 5.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; 2.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
```

```
KW   Laminin EGF-like domain.
FT   NON_TER       1      1
SQ   SEQUENCE   1806 AA;  199411 MW;  EF94CDE2AEA52B93 CRC64;

  Query Match             79.3%;  Score 3560.5;  DB 2;  Length 1806;
  Best Local Similarity   78.4%;  Pred. No. 2.5e-230;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||: |||||||:|||||||||||||:||||
Db        864 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 923

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        924 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 983

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db        984 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 1043

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||:||||:|| | | |||||||
Db       1044 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1103

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1104 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1163

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||||:|||||||||||||||
Db       1164 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1223

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||:|||||||:|||:| :| ||   | ||||||||||| ||:||
Db       1224 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1283

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1284 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1343

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| |||||||||
Db       1344 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1403

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1404 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1461

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| ||||||||||||::|:|||| :|||: |||:||:|||:: ||:||||
Db       1462 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1521

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       1522 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRARREGSLPGNSTISIRAPVYL 1581

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :||||||::|||:|||| :||: |||| |||| ||||||||: ||||
Db       1582 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1641

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || |||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1642 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1701

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:|||||||||||||:||| ||||
Db       1702 SVTPKQSLCDGQWHSVAVTIKQHILHL 1728


RESULT 8
Q76E14
ID   Q76E14      PRELIMINARY;      PRT;  3333 AA.
AC   Q76E14;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Laminin alpha 3b chain.
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kariya Y., Yasuda C., Nakashima Y., Ishida K., Tsubota Y.,
RA   Miyazaki K.;
RT   "Characterization of laminin 5B and NH2-terminal proteolytic fragment
RT   of its alpha3B chain: promotion of cellular adhesion, migration, and
RT   proliferation.";
RL   J. Biol. Chem. 279:24774-24784(2004).
DR   EMBL; AB107369; BAD13428.1; -.
DR   GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR   GO; GO:0005606; C:laminin-1; IEA.
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR008211; Laminin_N.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 8.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   Pfam; PF00055; Laminin_N; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   ProDom; PD003031; Laminin_B; 1.
DR   SMART; SM00181; EGF; 8.
DR   SMART; SM00180; EGF_Lam; 14.
DR   SMART; SM00281; LamB; 1.
DR   SMART; SM00282; LamG; 5.
DR   SMART; SM00136; LamNT; 1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; 12.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 13.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Laminin EGF-like domain.
SQ   SEQUENCE   3333 AA;  366616 MW;  6F99AF4D4B99FCB0 CRC64;

  Query Match .           79.3%;  Score 3560.5;  DB 2;  Length 3333;
  Best Local Similarity   78.4%;  Pred. No. 6.4e-230;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||: |||||||:|||||||||||||:||||
Db       2391 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 2450

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db       2451 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 2510

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db       2511 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 2570
```

```
Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||||  |||||||||||||||||||||||||||||||||:||||:||  |  |  |||||||
Db       2571 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 2630

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              ||||||||||  |  |||||||||  ||||||||||  |||:|:  |  ||:|:|||||  |  |||||
Db       2631 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 2690

Qy        301 KRMWINVVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::   |:||:|||||||||||||||||||||||||:|||||||||||||||
Db       2691 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 2750

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||:||||||||:|||:|  :|  ||   |  ||||||||||| ||:||
Db       2751 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 2810

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:|||||  ||   ||||||  ||||||||:||||||  ||||||||||:||
Db       2811 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 2870

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||||  :||||||||  |||  |  |||||||  |  |  |:|  ||||||||
Db       2871 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 2930

Qy        541 KPPPLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              |||||||  |   ||||  :  |  :|||:||  |  |:  ||  :  |||   :|  |   |:|:|  |||
Db       2931 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 2988

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              |||  ||||||  ||||||||||||||::|:||||  :||||:  |||:||:|||:::  ||:||||
Db       2989 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 3048

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||:  :||||||||||  :|  |  |||||||||:||||||||||  |   |||
Db       3049 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 3108

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | |  ||||||  :||||||::|||:||||  :||:  ||||  ||||  |||||||||:  ||||
Db       3109 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 3168

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:||  ||||  ||  ||||||||||:|||:|||  |:  |  ||:||||||  |:  |  |||: |
Db       3169 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 3228

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:|||||||||||||:||| ||||
Db       3229 SVTPKQSLCDGQWHSVAVTIKQHILHL 3255


RESULT 9
Q867A1
ID   Q867A1      PRELIMINARY;      PRT;  1725 AA.
AC   Q867A1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Laminin alpha 3 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Pissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Spirito F., Capt A., Guaguere E., Ortonne J.-P., Meneguzzi G.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF236865; AAL54876.1; -.
DR   HSSP; P11209; 1G2C.
DR   GO; GO:0005606; C:laminin-1; IEA.
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00053; Laminin_EGF; 2.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   SMART; SM00180; EGF_Lam; 2.
DR   SMART; SM00282; LamG; 5.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Laminin EGF-like domain.
FT   NON_TER    1725   1725
SQ   SEQUENCE   1725 AA;  191053 MW;  DF71EB0E1FB5134C CRC64;

  Query Match             74.2%;  Score 3331;  DB 2;  Length 1725;
  Best Local Similarity   73.2%;  Pred. No. 6.6e-215;
  Matches  635;  Conservative   98;  Mismatches  132;  Indels    2;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||| |||||: ||:| ||:|||||||||| |:||||
Db        782 MRFNGKSGVEVRLPNDLEDLKGYTSLSFFLQRPESRESGRTENMFVMYLGNKDISRDYIG 841

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||:||||||||::|:|:|:||  : :||:|||:|||||||||||||| |||||:|||:
Db        842 MAVVDGRLTCVYNLGEQESELQVDQSVIKSETQEAIMDRVKFQRIYQFASLNYTKKATSS 901

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              || :   :::: |:|:|||||||||: |||||||| || ||:|||||||||||||||||||
Db        902 KPGSSQFHEMDSGNSHTLLNLDPENTVFYVGGYPSDFTLPARLRFPPYKGCIELDDLNEN 961

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||:|||||||||:|||  |||  |||   ||||||
Db        962 VLSLYNFKKTFNLNTTEVEPCRRRKEESDRNYFEGTGYARVPTQLNAPNPNFGLTIQTTV 1021

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              ||||||||||| |||||||| |:|:||||||||||: |   :|||||  ||| ||| |
Db       1022 DRGLLFFAENQDRFISLNIEDGKLLVQYKLNSEPPKEREIGHIVNDGKDHRILIVIGKFQ 1081

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |: | |: :: :|:|:|||||||||||||||:||||||||||:|||||||||:|||||
Db       1082 NRISIAVSSQNSQIDGDIFDFSTYYLGGIPISIRERFNISTPAFRGCMKNLKKTTGVVRL 1141

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||:|||||  ||: || ||:|    || |||||||||| | | |
Db       1142 NDTVGVTKKCSEDWKLVRSASFSRDGQLRFTGLDLPLPSEFQASFGFQTFQPSGILFNLQ 1201

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              :    | ||||||||||:||:::: | :|| |||||  || ||||  | ||||||||| |:
Db       1202 SPKHYLQVTLEDGHIELNTRENSL-IIRSPQTYMDGELHFVSVIGDNSGLRLLIDDQTLK 1260

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ||:|   | :|  | |||  |||||||| :|| |:|| |||||||: |:| |||||||
Db       1261 SNQKLQDLSGSQHPLYLGGSQFEGCISNVFIQRVSKSPAVLDLASKTFKRDVSLGGCSLN 1320

Qy        541 KPPPLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              |||||||  :   | ||   ||:|| :|| | |:  || | |:: :|||||     |  |
Db       1321 KPPFLMLLRGSTRLNKSHTFNINQPLQDTPVASPRSMEMWREAQSCLPPPQAPTSPGAFS 1380

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              |||||||||   :||||:||||:|::|:|| | :||||| |||:|::|||:: ||::|||
Db       1381 FGDSPTSHLQFTIPQELVKPRSRFAVDVQTASSRGLVFYTGTKNSYMALYLSKGRLIFAL 1440

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |||||||||:|||: :|||||||||| :  |  |:||||||:|||||||| |     |||
Db       1441 GAGGKKLRLKSKEKCNDGKWHTVVFGQDDKKGHLIVDGLRAREGSLPGNSTFSLTAPVYL 1500
```

```
Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              |  . : |||||||:|||||||:|||: ||||:|||  ||||||||||||||||| ||||
Db       1501 GSSPAEKPKSLPQNSFVGCLRNFQLDLKPLDTPSASVGVSPCLGGSLEKGIYFSQEGGHV 1560

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              |||||| |||| || ||||||||||:|:||||| |: | ||||||||| || |:||| :|
Db       1561 ILANSVLLGPEFKLVFSIRPRSLTGILMHVGSQPGRYLCVYMEAGKVTASVDSEAGGILT 1620

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |||||||||||:|||| |:||| |:||
Db       1621 SITPKQSLCDGRWHSVTVTIKQHIVHL 1647


RESULT 10
LMA4_HUMAN
ID   LMA4_HUMAN     STANDARD;      PRT;  1816 AA.
AC   Q16363; Q14735; Q15335; Q9UE18; Q9UJN9;
DT   01-NOV-1997 (Rel. 35, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Laminin alpha-4 chain precursor.
GN   Name=LAMA4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal lung;
RX   MEDLINE=95300971; PubMed=7781776; DOI=10.1016/0014-5793(95)00462-I;
RA   Iivanainen A., Sainio K., Sariola H., Tryggvason K.;
RT   "Primary structure and expression of a novel human laminin alpha 4
RT   chain.";
RL   FEBS Lett. 365:183-188(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=97454279; PubMed=9310354;
RA   Richards A.J., Luccarini C., Pope F.M.;
RT   "The structural organisation of LAMA4, the gene encoding laminin
RT   alpha4.";
RL   Eur. J. Biochem. 248:15-23(1997).
RN   [3]
RP   SEQUENCE OF 236-1816 FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=95048381; PubMed=7959779;
RA   Richards A.J., Al-Imara L., Carter N.P., Lloyd J.C., Leversha M.A.,
RA   Pope F.M.;
RT   "Localization of the gene (LAMA4) to chromosome 6q21 and isolation of
RT   a partial cDNA encoding a variant laminin A chain.";
RL   Genomics 22:237-239(1994).
RN   [4]
RP   SEQUENCE OF 66-1816 FROM N.A.
RA   Tubby B.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC       is thought to mediate the attachment, migration and organization
CC       of cells into tissues during embryonic development by interacting
CC       with other extracellular matrix components.
CC   -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC       different polypeptide chains (alpha, beta, gamma), which are bound
CC       to each other by disulfide bonds into a cross-shaped molecule
CC       comprising one long and three short arms with globules at each
CC       end.
CC   -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC       membranes (major component).
CC   -!- TISSUE SPECIFICITY: In adult, strong expression in heart, lung,
CC       ovary small and large intestines, placenta, liver; weak or no
CC       expression in skeletal muscle, kidney, pancreas, testis, prostate,
CC       brain. High expression in fetal lung and kidney. Expression in
CC       fetal and newborn tissues is observed in certain mesenchymal cells
CC       in tissues such as smooth muscle and dermis.
CC   -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC       with other laminin chains to form a coiled coil structure.
CC   -!- DOMAIN: Domain G is globular.
CC   -!- SIMILARITY: Contains 4 laminin EGF-like domains.
CC   -!- SIMILARITY: Contains 5 laminin G-like domains.
CC   -!- CAUTION: Gene LAMA4 was formerly called LAMA3.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S78569; AAB34635.1; -.
DR   EMBL; X91171; CAA62596.1; -.
DR   EMBL; Y14240; CAA74636.1; -.
DR   EMBL; X76939; CAA54258.1; -.
DR   EMBL; Z99289; -; NOT_ANNOTATED_CDS.
DR   PIR; S68960; S68960.
DR   HSSP; P02468; 1NPE.
DR   Genew; HGNC:6484; LAMA4.
DR   MIM; 600133; -.
DR   GO; GO:0005605; C:basal lamina; TAS.
DR   GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00053; Laminin_EGF; 3.
DR   Pfam; PF00054; Laminin_G; 3.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
KW   Basement membrane; Cell adhesion; Coiled coil; Extracellular matrix;
KW   Glycoprotein; Laminin EGF-like domain; Repeat; Signal.
FT   SIGNAL        1     24       Potential.
FT   CHAIN        25   1816       Laminin alpha-4 chain.
FT   DOMAIN       82    131       Laminin EGF-like 1.
FT   DOMAIN      132    186       Laminin EGF-like 2.
FT   DOMAIN      187    240       Laminin EGF-like 3.
FT   DOMAIN      241    255       Laminin EGF-like 4 (incomplete).
FT   DOMAIN      256    825       Domain II and I.
FT   DOMAIN      826   1028       Laminin G-like 1.
FT   DOMAIN     1040   1220       Laminin G-like 2.
FT   DOMAIN     1227   1395       Laminin G-like 3.
FT   DOMAIN     1462   1633       Laminin G-like 4.
FT   DOMAIN     1640   1813       Laminin G-like 5.
FT   DOMAIN      313    396       Coiled coil (Potential).
FT   DOMAIN      466    521       Coiled coil (Potential).
FT   DOMAIN      574    607       Coiled coil (Potential).
FT   DOMAIN      655    717       Coiled coil (Potential).
FT   DOMAIN      770    799       Coiled coil (Potential).
FT   SITE        717    719       Cell attachment site (Potential).
FT   DISULFID     82     91       By similarity.
FT   DISULFID     84     98       By similarity.
FT   DISULFID    101    110       By similarity.
FT   DISULFID    113    129       By similarity.
FT   DISULFID    132    146       By similarity.
FT   DISULFID    134    155       By similarity.
FT   DISULFID    157    166       By similarity.
FT   DISULFID    169    184       By similarity.
FT   DISULFID    187    202       By similarity.
FT   DISULFID    189    209       By similarity.
FT   DISULFID    212    221       By similarity.
FT   DISULFID    224    238       By similarity.
FT   DISULFID    266    266       Interchain (Probable).
```

```
FT   DISULFID    269    269       Interchain (Probable).
FT   CARBOHYD    104    104       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    215    215       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    308    308       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    458    458       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    524    524       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    550    550       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    571    571       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    574    574       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    631    631       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    639    639       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    735    735       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    751    751       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    754    754       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    780    780       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    803    803       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1086   1086       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1281   1281       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1359   1359       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1411   1411       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT    143    143       A -> P (in Ref. 1).
FT   CONFLICT    178    178       L -> F (in Ref. 1).
FT   CONFLICT    265    265       G -> GMDCPTIS (in Ref. 4).
FT   CONFLICT    276    276       D -> A (in Ref. 4).
FT   CONFLICT    491    491       Y -> H (in Ref. 2 and 3).
FT   CONFLICT   1057   1057       T -> P (in Ref. 1).
FT   CONFLICT   1110   1112       SGR -> GGP (in Ref. 4).
SQ   SEQUENCE   1816 AA;  201908 MW;  04E9AF379A0F4A4D CRC64;

  Query Match             26.5%;  Score 1190;  DB 1;  Length 1816;
  Best Local Similarity   33.2%;  Pred. No. 1.1e-70;
  Matches  310;  Conservative  161;  Mismatches  372;  Indels   90;  Gaps   27;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFL----QRPDLRENGGTEDMFVMYLGNKDASK 56
              | |:|:| |||     ::||| :|||||::    :||:| |    | | |::|||:|:| |
Db        829 MMFDGQSAVEVHSRTSMDDLKAFTSLSLYMKPPVKRPELTE---TADQFILYLGSKNAKK 885

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
             :|:|:|: :   |  ||||| :: |: :|        | |     || :|: :  |:  |
Db        886 EYMGLAIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVP 943

Qy        117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDD 176
              : |:  :   :    |    ::||:|||| |||||| | :|:||: |  | : ||:||
Db        944 SLSSTAEEKFIKKGEFSGDDSLLDLDPEDTVFYVGGVPSNFKLPTSLNLPGFVGCLELAT 1003

Qy        177 LNENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYA--RIPTQPN--A 227
              || :|:|||||  :|:: :   || | |       :   :|:|:||  |  |:
Db       1004 LNNDVISLYNFKHIYNMDPSTSVPCARDKLAFTQSRAASYFFDGSGYAVVRDITRRGKFG 1063

Qy        228 PFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRY-------KLNSEPPKEKGI 280
                |   ::|  | ||:    |   | | : :| | | |       ::: |   :|
Db       1064 QVTRFDIEVRTPADNGLILLMVNGSMFFRLEMRNGYLHVFYDFGFSSGRVHLEDTLKKA- 1122

Qy        281 RDTINDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIP------I 331
               ||| | | | |     |:| : |: | |:    |     |:  |:|| |
Db       1123 --QINDAKYHEISI-IYHNDKKMILVVDRRHVKSMDNEKMKIPFTDIYIGGAPPEILQSR 1179

Qy        332 AIRERFNISTPAFQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQM 388
              |:|    :    |:|||      ||   ::   :|:||   | ||  : | |:  ||
Db       1180 ALRAHLPLDI-NFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQS 1236

Qy        389 SFTNLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIF 447
                ::  :   | |:  | |:| ||:| |  : : :    ::|::| : :  :   | :
Db       1237 FIASIQKISFFDGFEGGFNFRTLQPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQ 1294

Qy        448 KSPGTYMDGLLHHVSVISDTSGLR--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-- 499
                | ||| |   |||  |  |  |::|  :|  :|       | | :    ||
Db       1295 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSP 1352

Qy        500 -----GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
                  :| |||||    |  :  || |    : |   ||  | :   |  :| | |
Db       1353 ISAQYANFTGCISNAYFTRVDRDVEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNL 1412

Qy        555 NKGRIFNVNQ--LMQDAPQATRSTEAWQDGRSCLPPLNT-----------KASHRALQF 600
              :| :    :   :|||       :|      ||  ||            :|   | |:
Db       1413 SKPKASQNKKGGKSKDAP-------SWDPVALKLPERNTPRNSHCHLSNSPRAIEHAYQY 1465

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKD--SFLALYVADGRVVFA 658
              | :  |    :  :     :||||: ::| |  |::||   ::   |: |::| ||:|:
Db       1466 GGTANSRQEFEHLKGDFGAKSQFSIRLRTRSSHGMIFYVSDQEENDFMTLFLAHGRLVYM 1525

Qy        659 LGAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSL-PGNSTISPREQV 717
                | |||::||:|:|:|| || |:|      |||:|||| | || | :|   :  :
Db       1526 FNVGHKKLKIRSQEKYNDGLWHDVIFIRERSSGRLVIDGLRVLEESLPPTEATWKIKGPI 1585

Qy        718 YLGLPLSRKPKSLPQ----HSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFS 773
              |||      |      |    :|| ||| : |||   : | |  | |:||  | :| | |||
Db       1586 YLGGVAPGKAVKNVQINSIYSFSGCLSNLQLNGASITSASQTFSVTPCFEGPMETGTYFS 1645

Qy        774 QGGGHVILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSD 833
                ||:|:|  | ::| : :: | :|||| :| |:|  | :|: |:|:|: |:|   |::
Db       1646 TEGGYVVLDESFNIGLKFEIAFEVRPRSSSGTLVHGHSVNGEYLNVHMKNGQVIVKVNNG 1705

Qy        834 AGGSVTSITPKQSLCDGQWHSVAVSIKQRILHL 866
                ||:||||||||:|| : |     :: |
Db       1706 IRDFSTSVTPKQSLCDGRWHRITVIRDSNVVQL 1738


RESULT 11
Q91VV0
ID   Q91VV0      PRELIMINARY;      PRT;  1254 AA.
AC   Q91VV0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Lama4 protein (Fragment).
GN   Name=Lama4;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC008533; AAH08533.1; -.
DR   HSSP; Q60675; 1QU0.
DR   MGD; MGI:109321; Lama4.
DR   GO; GO:0005605; C:basal lamina; IDA.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0001568; P:blood vessel development; IMP.
```

```
DR   Pfam; PF02210; Laminin_G_2; 5.
DR   Pfam; PF06009; Laminin_II; 1.
DR   SMART; SM00282; LamG; 5.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
FT   NON_TER      1      1
SQ   SEQUENCE   1254 AA;  139723 MW;  54D49EF763D37CD9 CRC64;

  Query Match             26.4%;  Score 1185;  DB 2;  Length 1254;
  Best Local Similarity   32.8%;  Pred. No. 1.4e-70;
  Matches  305;  Conservative  164;  Mismatches  378;  Indels   82;  Gaps   26;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQ---RPDLRENGGTEDMFVMYLGNKDASKD 57
              | |:|:| |||     ::||| :||:||:::   :|          | ||:|||:|:| |:
Db        267 MMFDGQSAVEVHPKVSVDDLKAFTSISLYMKPPPKPAEPTGAWVADQFVLYLGSKNAKKE 326

Qy         58 YIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEA 117
              |:|:|: :   |  ||||| :: |: :|        |  |     || :|: :  |: |  :
Db        327 YMGLAIKNDNLVYVYNLGMKDVEILLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVPS 384

Qy        118 TSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDL 177
               |:  :   :   |     ::||:| ||| |||||| | :|:||: |  | | ||:||  |
Db        385 LSSTAEEKFIKKGEFAGDDSLLDLTPEDTVFYVGGVPANFKLPASLNLPSYSGCLELATL 444

Qy        178 NENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYA--RIPTQPN--AP 228
              | :|:|||||  :|:: ::  || | |       :   :|:|: ||   |  |:
Db        445 NNDVISLYNFKHIYNMDPSKSVPCARDKLAFTQSRAASYFFDGSSYAVVRDITRRGKFGQ 504

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLN-SEPPKEKGIRDT---- 283
                |   |:|  | ||:    |  | || : :| | | |     |  |    : ||
Db        505 VTRFDIEIRTPADNGLVLLMVNGSMFFSLEMRNGYLHVFYDFGFSNGPVH--LEDTLKKA 562

Qy        284 -INDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIPIAIRERFNI 339
               ||| | | | | |    |:| : |: | |:    | :   |:  |:|| |  : :   :
Db        563 QINDAKYHEISI-IYHNDKKMILVVDRRHVKSTDNEKKKIPFTDIYIGGAPQEVLQSRTL 621

Qy        340 STPA-----FQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFT 391
                    |:||||     ||   ::   :|:||   | ||  : | | |:  ||
Db        622 RAHLPLDINFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIA 679

Qy        392 NLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSP 450
              ::  :   | |:  | |:| ||:| |  : : :    ::|::| : :  :   | : :
Db        680 SIQKISFFDGFEGGFNFRTLQPNGLLFYYTSGSDVFSISLDNGTVVMDVK--GIKVMSTD 737

Qy        451 GTYMDGLLHH-VSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQQS------LRLGG---- 499
              | ||| |  |: ||||    |::|   ||      |:   |:|:          ||
Db        738 KQYHDGLPHFVVTSISDTR-YELVVDKSRLRGKN--PTKGKAEQTQTTEKKFYFGGSPIS 794

Qy        500 ---GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 556
                :| |||||    |  :  || |    | |   ||  | :   |  :| |  | :|
Db        795 PQYANFTGCISNAYFTRLDRDVEVEDFQRYSEKVHTSLYECPIESSPLFLLHKKGKNSSK 854

Qy        557 GRIFNVNQLMQDAP-----------QATRSTEAWQDGRSCLPPLNTKASHRALQFGDSP 604
              :    :  :|||            :| | :       |     : :|    | |:| :
Db        855 PKTNKQGEKSKDAPSWDPIGLKFLEQKAPRDSH-------CHLSSSPRAIEHAYQYGGTA 907

Qy        605 TSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKD--SFLALYVADGRVVFALGAG 662
              |    :  |     :|||:: ::| |  |::||   ::   |: |::| ||:||     |
Db        908 NSRQEFEHEQGDFGEKSQFAIRLKTRSSHGMIFYVSDQEENDFMTLFLAHGRLVFMFNVG 967

Qy        663 GKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSL-PGNSTISPREQVYL-G 720
              |||::||:|:|:|| || |:|       |||:|||| |  | |  :    :  :|| |
Db        968 HKKLKIRSQEKYNDGLWHDVIFIREKSSGRLVIDGLRVLEERLPPSGAAWKIKGPIYLGG 1027

Qy        721 LPLSRKPKSL---PQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGG 777
              :   |  |::     :|| ||| : |||    : | |  | |:||  | :| | |||  ||
Db       1028 VAPGRAVKNVQITSVYSFSGCLGNLQLNGASITSASQTFSVTPCFEGPMETGTYFSTEGG 1087

Qy        778 HVILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGS 837
              :|:|  | ::| : :: | :|||| :| |:|  | :|: |:|:|  |:|   |::
Db       1088 YVVLDESFNIGLKFEIAFEVRPRSSSGTLVHGHSVNGEYLNVHMRNGQVIVKVNNGVRDF 1147

Qy        838 VTSITPKQSLCDGQWHSVAVSIKQRILHL 866
               ||:||||:||||:|| : |     :: |
Db       1148 STSVTPKQNLCDGRWHRITVIRDSNVVQL 1176


RESULT 12
LMA4_MOUSE
ID   LMA4_MOUSE     STANDARD;      PRT;  1816 AA.
AC   P97927; O88785; P70409;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Laminin alpha-4 chain precursor.
GN   Name=Lama4;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 462-469; 478-483; 776-782 AND
RP   940-945.
RC   STRAIN=BALB/c; TISSUE=Endothelial cells;
RX   MEDLINE=97363207; PubMed=9219532;
RA   Frieser M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,
RA   Sorokin L.M.;
RT   "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of
RT   endothelium.";
RL   Eur. J. Biochem. 246:727-735(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=97202462; PubMed=9049981; DOI=10.1016/S0945-053X(96)90162-6;
RA   Liu J., Mayne R.;
RT   "The complete cDNA coding sequence and tissue-specific expression of
RT   the mouse laminin alpha 4 chain.";
RL   Matrix Biol. 15:433-437(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=98010627; PubMed=9346933; DOI=10.1074/jbc.272.44.27862;
RA   Iivanainen A., Kortesmaa J., Sahlberg C., Morita T., Bergmann U.,
RA   Thesleff I., Tryggvason K.;
RT   "Primary structure, developmental expression, and immunolocalization
RT   of the murine laminin alpha4 chain.";
RL   J. Biol. Chem. 272:27862-27868(1997).
RN   [4]
RP   SEQUENCE OF 836-1106 FROM N.A.
RC   STRAIN=ICR; TISSUE=Placenta;
RX   MEDLINE=97296337; PubMed=9151674; DOI=10.1083/jcb.137.3.685;
RA   Miner J.H., Patton B.L., Lentz S.I., Gilbert D.J., Snider W.D.,
RA   Jenkins N.A., Copeland N.G., Sanes J.R.;
RT   "The laminin alpha chains: expression, developmental transitions, and
RT   chromosomal locations of alpha1-5, identification of heterotrimeric
RT   laminins 8-11, and cloning of a novel alpha3 isoform.";
RL   J. Cell Biol. 137:685-702(1997).
RN   [5]
RP   SEQUENCE OF 1467-1691 FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=97187457; PubMed=9034910;
RX   DOI=10.1002/(SICI)1096-9861(19970224)378:4<547::AID-CNE9>3.0.CO;2-2;
RA   Lentz S.I., Miner J.H., Sanes J.R., Snider W.D.;
RT   "Distribution of the ten known laminin chains in the pathways and
RT   targets of developing sensory axons.";
RL   J. Comp. Neurol. 378:547-561(1997).
CC   -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC       is thought to mediate the attachment, migration and organization
CC       of cells into tissues during embryonic development by interacting
CC       with other extracellular matrix components.
CC   -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC       different polypeptide chains (alpha, beta, gamma), which are bound
CC       to each other by disulfide bonds into a cross-shaped molecule
CC       comprising one long and three short arms with globules at each
CC       end.
CC   -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC       membranes (major component).
```

```
CC   -!- TISSUE SPECIFICITY: Strongly expressed in peripheral nerves,
CC       cardiac muscle, fat, dermis, lung stroma, aortic endothelium,
CC       endocardium and endothelium of blood vessels in skin and brain.
CC   -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC       with other laminin chains to form a coiled coil structure.
CC   -!- DOMAIN: Domain G is globular.
CC   -!- SIMILARITY: Contains 4 laminin EGF-like domains.
CC   -!- SIMILARITY: Contains 5 laminin G-like domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U58950; AAB41840.1; -.
DR   EMBL; Y09827; CAA70970.1; -.
DR   EMBL; U59865; AAC24725.1; -.
DR   EMBL; U88352; AAC53178.1; -.
DR   EMBL; U69176; AAC52982.1; -.
DR   HSSP; P02468; 1NPE.
DR   MGD; MGI:109321; Lama4.
DR   GO; GO:0005604; C:basement membrane; IDA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00053; Laminin_EGF; 3.
DR   Pfam; PF00054; Laminin_G; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Basement membrane; Cell adhesion; Coiled coil;
KW   Direct protein sequencing; Extracellular matrix; Glycoprotein;
KW   Laminin EGF-like domain; Repeat; Signal.
FT   SIGNAL       1     24       Potential.
FT   CHAIN       25   1816       Laminin alpha-4 chain.
FT   DOMAIN      82    131       Laminin EGF-like 1.
FT   DOMAIN     132    186       Laminin EGF-like 2.
FT   DOMAIN     187    240       Laminin EGF-like 3.
FT   DOMAIN     241    255       Laminin EGF-like 4 (incomplete).
FT   DOMAIN     256    825       Domain II and I.
FT   DOMAIN     826   1030       Laminin G-like 1.
FT   DOMAIN    1042   1222       Laminin G-like 2.
FT   DOMAIN    1229   1397       Laminin G-like 3.
FT   DOMAIN    1462   1633       Laminin G-like 4.
FT   DOMAIN    1640   1813       Laminin G-like 5.
FT   DOMAIN     431    523       Coiled coil (Potential).
FT   DOMAIN     556    604       Coiled coil (Potential).
FT   DOMAIN     655    717       Coiled coil (Potential).
FT   DOMAIN     770    799       Coiled coil (Potential).
FT   SITE       717    719       Cell attachment site (Potential).
FT   DISULFID    82     91       By similarity.
FT   DISULFID    84     98       By similarity.
FT   DISULFID   101    110       By similarity.
FT   DISULFID   113    129       By similarity.
FT   DISULFID   132    146       By similarity.
FT   DISULFID   134    155       By similarity.
FT   DISULFID   157    166       By similarity.
FT   DISULFID   169    184       By similarity.
FT   DISULFID   187    202       By similarity.
FT   DISULFID   189    209       By similarity.
FT   DISULFID   212    221       By similarity.
FT   DISULFID   224    238       By similarity.
FT   DISULFID   266    266       Interchain (Probable).
FT   DISULFID   269    269       Interchain (Probable).
FT   CARBOHYD   104    104       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   215    215       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   308    308       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   333    333       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   458    458       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   550    550       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   571    571       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   574    574       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   631    631       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   639    639       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   735    735       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   751    751       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   754    754       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   780    780       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   803    803       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1088   1088       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1283   1283       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1361   1361       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT     8      8       C -> S (in Ref. 2).
FT   CONFLICT    18     18       C -> Y (in Ref. 2).
FT   CONFLICT   248    248       C -> R (in Ref. 3).
FT   CONFLICT   297    297       G -> A (in Ref. 3).
FT   CONFLICT   431    433       THR -> HPS (in Ref. 2).
FT   CONFLICT   679    679       S -> C (in Ref. 3).
FT   CONFLICT   703    703       D -> G (in Ref. 2).
FT   CONFLICT   706    706       N -> H (in Ref. 2).
FT   CONFLICT   728    728       K -> R (in Ref. 2).
FT   CONFLICT   730    730       F -> I (in Ref. 2).
FT   CONFLICT   779    779       R -> G (in Ref. 1; AA sequence).
FT   CONFLICT   810    810       R -> S (in Ref. 3).
FT   CONFLICT   865    867       AEP -> QT (in Ref. 2).
FT   CONFLICT   936    936       K -> E (in Ref. 3).
FT   CONFLICT   970    970       L -> V (in Ref. 3).
FT   CONFLICT  1132   1132       H -> R (in Ref. 2).
FT   CONFLICT  1200   1200       F -> I (in Ref. 2).
FT   CONFLICT  1382   1382       D -> A (in Ref. 2).
FT   CONFLICT  1413   1414       NS -> EF (in Ref. 1).
FT   CONFLICT  1489   1489       A -> S (in Ref. 2).
SQ   SEQUENCE  1816 AA;  201818 MW;  B49C45F3A45999D8 CRC64;
```

```
  Query Match             26.4%;  Score 1185;  DB 1;  Length 1816;
  Best Local Similarity   32.8%;  Pred. No. 2.4e-70;
  Matches  305;  Conservative  164;  Mismatches  378;  Indels   82;  Gaps   26;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQ---RPDLRENGGTEDMFVMYLGNKDASKD 57
              | |:|:| |||     ::||| :||:||:::   :|          | ||:|||:|:| |:
Db        829 MMFDGQSAVEVHPKVSVDDLKAFTSISLYMKPPPKPAEPTGAWVADQFVLYLGSKNAKKE 888

Qy         58 YIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEA 117
              |:|:|: :  |  ||||| :: |: :|       | |     || :|: :  |:  |  :
Db        889 YMGLAIKNDNLVYVYNLGMKDVEILLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVPS 946

Qy        118 TSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDL 177
              |:  :   :  |    ::||:| ||| |||||| | :|:||: |  | | ||:|| |
Db        947 LSSTAEEKFIKKGEFAGDDSLLDLTPEDTVFYVGGVPANFKLPASLNLPSYSGCLELATL 1006

Qy        178 NENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYA--RIPTQPN--AP 228
              | :|:|||||| :|:: ::  || | |       :   :|:|: ||  |  |:
Db       1007 NNDVISLYNFKHIYNMDPSKSVPCARDKLAFTQSRAASYFFDGSSYAVVRDITRRGKFGQ 1066

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLN-SEPPKEKGIRDT---- 283
                |   |:|  | ||:    |   | || : :| | | |    | |    : ||
Db       1067 VTRFDIEIRTPADNGLVLLMVNGSMFFSLEMRNGYLHVFYDFGFSNGPVH--LEDTLKKA 1124

Qy        284 -INDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIPIAIRERFNI 339
               ||| | | | | |    |:| : |: | |:    | :   |:  |:|| |  : :   :
Db       1125 QINDAKYHEISI-IYHNDKKMILVVDRRHVKSTDNEKKKIPFTDIYIGGAPQEVLQSRTL 1183

Qy        340 STPA-----FQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFT 391
                      |:||||     ||   ::   :|:||   | ||  : | | |:  ||
Db       1184 RAHLPLDINFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIA 1241
```

```
Qy        392 NLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSP 450
              ::  :   | |:  | |:| ||:| |  : : :    ::|::| : :  :   | :  :
Db       1242 SIQKISFFDGFEGGFNFRTLQPNGLLFYYTSGSDVFSISLDNGTVVMDVK--GIKVMSTD 1299

Qy        451 GTYMDGLLHH-VSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQQS------LRLGG---- 499
              | ||| |  |: ||||    |::|   ||     |:   |:|:           ||
Db       1300 KQYHDGLPHFVVTSISDTR-YELVVDKSRLRGKN--PTKGKAEQTQTTEKKFYFGGSPIS 1356

Qy        500 ---GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 556
                :| |||||    |  :  || |    | |   ||  | :   |  :| |  |  :|
Db       1357 PQYANFTGCISNAYFTRLDRDVEVEDFQRYSEKVHTSLYECPIESSPLFLLHKKGKNSSK 1416

Qy        557 GRIFNVNQLMQDAP-----------QATRSTEAWQDGRSCLPPLNTKASHRALQFGDSP 604
               :    :  :|||            :| | :         |    : :|   | |:| :
Db       1417 PKTNKQGEKSKDAPSWDPIGLKFLEQKAPRDSH-------CHLSSSPRAIEHAYQYGGTA 1469

Qy        605 TSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKD--SFLALYVADGRVVFALGAG 662
              |   :  |     :|||:: ::| |  |::||   ::   |: |::| ||:||    |
Db       1470 NSRQEFEHEQGDFGEKSQFAIRLKTRSSHGMIFYVSDQEENDFMTLFLAHGRLVFMFNVG 1529

Qy        663 GKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSL-PGNSTISPREQVYL-G 720
              |||::||:|:|:|| || |:|       |||:|||| |  | |  :   :  :|| |
Db       1530 HKKLKIRSQEKYNDGLWHDVIFIREKSSGRLVIDGLRVLEERLPPSGAAWKIKGPIYLGG 1589

Qy        721 LPLSRKPKSL---PQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGG 777
              :   |  |::     :|| ||| : |||   : | |  | |:||  | :| | |||  ||
Db       1590 VAPGRAVKNVQITSVYSFSGCLGNLQLNGASITSASQTFSVTPCFEGPMETGTYFSTEGG 1649

Qy        778 HVILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGS 837
              :|:|  | ::| : :: | :|||| :| |:|  | :|: |:|:|  |:|   |::
Db       1650 YVVLDESFNIGLKFEIAFEVRPRSSSGTLVHGHSVNGEYLNVHMRNGQVIVKVNNGVRDF 1709

Qy        838 VTSITPKQSLCDGQWHSVAVSIKQRILHL 866
              ||:||||:||||:|| : |     :: |
Db       1710 STSVTPKQNLCDGRWHRITVIRDSNVVQL 1738


RESULT 13
LMA5_HUMAN
ID   LMA5_HUMAN     STANDARD;      PRT;  3695 AA.
AC   O15230; Q8WZA7; Q9H1P1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Laminin alpha-5 chain precursor.
GN   Name=LAMA5; Synonyms=KIAA0533, KIAA1907;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA   Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA   Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
RN   [2]
RP   SEQUENCE OF 197-1934 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21456161; PubMed=11572484;
RA   Nagase T., Kikuno R., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XXI.
RT   The complete sequences of 60 new cDNA clones from brain which code for
RT   large proteins.";
RL   DNA Res. 8:179-187(2001).
RN   [3]
RP   SEQUENCE OF 2051-3695 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98290545; PubMed=9628581;
RA   Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RA   Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. IX.
RT   The complete sequences of 100 new cDNA clones from brain which can
RT   code for large proteins in vitro.";
RL   DNA Res. 5:31-39(1998).
RN   [4]
RP   SEQUENCE OF 2743-3695 FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=97415425; PubMed=9271224; DOI=10.1016/S0014-5793(97)00686-8;
RA   Durkin M.E., Loechel F., Mattei M.-G., Gilpin B.J., Albrechtsen R.,
RA   Wewer U.M.;
RT   "Tissue-specific expression of the human laminin alpha5-chain, and
RT   mapping of the gene to human chromosome 20q13.2-13.3 and to distal
RT   mouse chromosome 2 near the locus for the ragged (Ra) mutation.";
RL   FEBS Lett. 411:296-300(1997).
RN   [5]
RP   EXPRESSION IN RETINA.
RX   MEDLINE=20422761; PubMed=10964957;
RA   Libby R.T., Champliaud M.-F., Claudepierre T., Xu Y., Gibbons E.P.,
RA   Koch M., Burgeson R.E., Hunter D.D., Brunken W.J.;
RT   "Laminin expression in adult and developing retinae: evidence of two
RT   novel CNS laminins.";
RL   J. Neurosci. 20:6517-6528(2000).
CC   -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC       is thought to mediate the attachment, migration and organization
CC       of cells into tissues during embryonic development by interacting
CC       with other extracellular matrix components.
CC   -!- SUBUNIT: Laminin-15 complex is an heterotrimer composed of three
CC       chains (alpha-5/beta-2/gamma-3) which are bound to each other by
CC       disulfide bonds into a cross-shaped molecule comprising one long
CC       and three short arms with globules at each end.
CC   -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC       membranes (major component).
CC   -!- TISSUE SPECIFICITY: Expressed in heart, lung, kidney, skeletal
CC       muscle, pancreas, retina and placenta. Little or no expression in
CC       brain and liver.
CC   -!- DOMAIN: Domain G is globular and is part of the major cell-binding
CC       site located in the long arm of the laminin heterotrimer.
CC   -!- SIMILARITY: Contains 22 laminin EGF-like domains.
CC   -!- SIMILARITY: Contains 5 laminin G-like domains.
CC   -!- SIMILARITY: Contains 2 laminin IV domains.
CC   -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AL354836; CAC22309.1; ALT_SEQ.
```

```
DR   EMBL; AL354836; CAC22310.1; -.
DR   EMBL; AB067494; BAB67800.1; -.
DR   EMBL; AB011105; BAA25459.1; -.
DR   EMBL; Z95636; CAB09137.1; -.
DR   HSSP; P02468; 1NPE.
DR   Genew; HGNC:6485; LAMA5.
DR   MIM; 601033; -.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR008211; Laminin_N.
DR   InterPro; IPR008212; Lam_N2.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 18.
DR   Pfam; PF00054; Laminin_G; 2.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   Pfam; PF00055; Laminin_N; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   ProDom; PD003031; Laminin_B; 1.
DR   PROSITE; PS00022; EGF_1; 19.
DR   PROSITE; PS01186; EGF_2; 3.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Basement membrane; Cell adhesion; Coiled coil; Extracellular matrix;
KW   Glycoprotein; Laminin EGF-like domain; Repeat; Signal.
FT   SIGNAL       1     35       Potential.
FT   CHAIN       36   3695       Laminin alpha-5 chain.
FT   DOMAIN      36    299       Laminin N-terminal (domain VI).
FT   DOMAIN     300    358       Laminin EGF-like 1.
FT   DOMAIN     359    428       Laminin EGF-like 2.
FT   DOMAIN     429    474       Laminin EGF-like 3.
FT   DOMAIN     494    540       Laminin EGF-like 4.
FT   DOMAIN     541    586       Laminin EGF-like 5.
FT   DOMAIN     587    631       Laminin EGF-like 6.
FT   DOMAIN     632    676       Laminin EGF-like 7.
FT   DOMAIN     677    722       Laminin EGF-like 8.
FT   DOMAIN     723    775       Laminin EGF-like 9.
FT   DOMAIN     776    828       Laminin EGF-like 10.
FT   DOMAIN     829    850       Laminin EGF-like 11 (incomplete).
FT   DOMAIN     851   1437       Laminin domain IV 1 (domain IV B).
FT   DOMAIN    1438   1483       Laminin EGF-like 12.
FT   DOMAIN    1484   1527       Laminin EGF-like 13.
FT   DOMAIN    1528   1576       Laminin EGF-like 14.
FT   DOMAIN    1577   1627       Laminin EGF-like 15.
FT   DOMAIN    1628   1637       Laminin EGF-like 16 (N-terminal).
FT   DOMAIN    1638   1830       Laminin domain IV 2 (domain IV A).
FT   DOMAIN    1831   1863       Laminin EGF-like 16 (C-terminal).
FT   DOMAIN    1864   1912       Laminin EGF-like 17.
FT   DOMAIN    1913   1968       Laminin EGF-like 18.
FT   DOMAIN    1969   2022       Laminin EGF-like 19.
FT   DOMAIN    2023   2069       Laminin EGF-like 20.
FT   DOMAIN    2070   2116       Laminin EGF-like 21.
FT   DOMAIN    2117   2166       Laminin EGF-like 22.
FT   DOMAIN    2167   2735       Domain II and I.
FT   DOMAIN    2736   2929       Laminin G-like 1.
FT   DOMAIN    2941   3115       Laminin G-like 2.
FT   DOMAIN    3124   3292       Laminin G-like 3.
FT   DOMAIN    3340   3513       Laminin G-like 4.
FT   DOMAIN    3520   3692       Laminin G-like 5.
FT   DOMAIN    2203   2221       Coiled coil (Potential).
FT   DOMAIN    2335   2466       Coiled coil (Potential).
FT   DOMAIN    2510   2670       Coiled coil (Potential).
FT   SITE      1722   1724       Cell attachment site (Potential).
FT   SITE      1838   1840       Cell attachment site (Potential).
FT   DISULFID   300    309       By similarity.
FT   DISULFID   302    322       By similarity.
FT   DISULFID   324    333       By similarity.
FT   DISULFID   336    356       By similarity.
FT   DISULFID   359    368       By similarity.
FT   DISULFID   361    393       By similarity.
FT   DISULFID   396    405       By similarity.
FT   DISULFID   408    426       By similarity.
FT   DISULFID   429    440       By similarity.
FT   DISULFID   431    447       By similarity.
FT   DISULFID   449    458       By similarity.
FT   DISULFID   461    471       By similarity.
FT   DISULFID   494    506       By similarity.
FT   DISULFID   496    515       By similarity.
FT   DISULFID   517    526       By similarity.
FT   DISULFID   529    538       By similarity.
FT   DISULFID   541    553       By similarity.
FT   DISULFID   543    560       By similarity.
FT   DISULFID   562    571       By similarity.
FT   DISULFID   574    584       By similarity.
FT   DISULFID   587    599       By similarity.

  Query Match           23.2%;  Score 1042.5;  DB 1;  Length 3695;
  Best Local Similarity  31.6%;  Pred. No. 2.9e-60;
  Matches  294;  Conservative  159;  Mismatches  367;  Indels  109;  Gaps   32;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |:|||:|||::| | || ||  ||:|  :|| |:     |||| ||||:|:: |: ||:|
Db       2737 MKFNGRSGVQLRTPRDLADLAAYTALKFYLQGPEPEPGQGTEDRFVMYMGSRQATGDYMG 2796

Qy         61 MAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE--- 116
              ::: | ::  || ||:   | : ||: : |          |   |  ||  :: | |
Db       2797 VSLRDKKVHWVYQLGEAGPAVLSIDEDIGEQ------FAAVSLDRTLQFGHMSVTVERQM 2850

Qy        117 --ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIEL 174
                |     ||     ||     |||| |:| |||||||  |  |  |||| |:||||:
Db       2851 IQETKGDTVAPGA---EG-----LLNLRPDDFVFYVGGYPSTFTPPPLLRFPGYRGCIEM 2902

Qy        175 DDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPN-AP 228
              | ||| |:|||||: || |:|    || | |        :| :| :|||:|||      :
Db       2903 DTLNEEVVSLYNFERTFQLDTAVDRPCARSKSTGDPWLTDGSYLDGTGFARISFDSQIST 2962

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPP----- 275
              | | ::     |:||| : |  |: | :::|:|:: |   :        :||
Db       2963 TKRFEQELRLVSYSGVLFFLKQQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPPLTS 3022

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNER---SVRIEGEIFDFSTYYLGGI--- 329
              | |:           :  :|  :||: : |       ||  : ::     |||||:
Db       3023 ASKAIQ----------VFLLGGSRKRVLVRVERATVYSVEQDNDLELADAYYLGGVPPD 3071

Qy        330 --PIAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSR 384
                | ::|  |  :  : :||:| :|   |   : ||| | ||:  |: |  : |  :|
Db       3072 QLPPSLRWLFP-TGGSVRGCVKGIKALGKYVDLKRLN-TTGVSAGCTADLLVGRAMTFHG 3129

Qy        385 GG--QMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDS 442
              |  ::: :|:  | |      ||| : | |   |      :      |:|: | : |    :
Db       3130 HGFLRLALSNV-APLTGNVYSGFGFHSAQDSALLYYRASPDGLCQVSLQQGRVSLQLLRT 3188

Qy        443 NIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQV--LRRNQRLPSFSNAQQS----LR 496
              :   |:   : ||  |:|:  |: :|: | :|||:  :: :: |      |      |
Db       3189 EV---KTQAGFADGAPHYVAFYSNATGVWLYVDDQLQQMKPHRGPPPELQPQPEGPPRLL 3245

Qy        497 LGG-------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFK 549
              |||        :| |||||| |||       | ||       : |  ||:    | |   :
Db       3246 LGGLPESGTIYNFSGCISNVFVQRLLGPQRVFDLQQNLGSVNVST-GCA----PALQA-Q 3299

Qy        550 SPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQFGDSPTSHLL 609
              :|   :|       |   | :|:| :      :|: | : : :  : ||| | :||
Db       3300 TPGLGPRG-------LQATARKASRRSRQPARHPACMLPPHLRTTRDSYQFGGSLSSH-- 3350

Qy        610 LKLPQELLKPRS--QFSLDIQTTSPKGLVFYAG---TKDSFLALYVADGRVVFALGAGGK 664
              |:    | : |:    |: :   | :||: :          |||::::|  |  :   |
Db       3351 LEFVGILARHRNWPSLSMHVLPRSSRGLLLFTARLRPGSPSLALFLSNGHFVAQMEGLGT 3410
```

```
Qy        665 KLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRA--QEG---SLPGNSTISPREQVYL 719
              :|| :|::|   |:|| |       :  || || ||  |||      |      |
Db       3411 RLRAQSRQRSRPGRWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHQGAEHPQPHTLFVG 3470

Qy        720 GLPLSRKPKSLP-QHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGH 778
              ||| |     ||    | ||::  :|: :|| :|:   ||:||: | || |::|   ||
Db       3471 GLPASSHSSKLPVTVGFSGCVKRLRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGV 3530

Qy        779 VILANSVSLGPELKLTFSIRPRSLTGVLIHVG-SQSGQRLSVYMEAGKVTTSVSSDAGGS 837
              : |    :  |:: |   :|| ::||:: |:| :::   | : :   :|       ||
Db       3531 ITLDLPGATLPDVGLELEVRPLAVTGLIFHLGQARTPPYLQLQVTEKQVLLRADDGAGEF 3590

Qy        838 VTSITPKQSLCDGQWHSVAVSIKQRILHL 866
               ||:|    ||||||| :||     :| |
Db       3591 STSVTRPSVLCDGQWHRLAVMKSGNVLRL 3619


RESULT 14
Q8TDF8
ID   Q8TDF8      PRELIMINARY;      PRT;  3695 AA.
AC   Q8TDF8;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Laminin alpha5 chain precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21935381; PubMed=11821406; DOI=10.1074/jbc.M111228200;
RA   Doi M., Thyboll J., Kortesmaa J., Jansson K., Iivanainen A.,
RA   Parvardeh M., Timpl R., Hedin U., Swedenborg J., Tryggvason K.;
RT   "Recombinant human laminin-10 (alpha5beta1gamma1). Production,
RT   purification, and migration-promoting activity on vascular endothelial
RT   cells.";
RL   J. Biol. Chem. 277:12741-12748(2002).
DR   EMBL; AF443072; AAM12527.1; -.
DR   HSSP; P02468; 1NPE.
DR   GO; GO:0005605; C:basal lamina; NAS.
DR   GO; GO:0005178; F:integrin binding; IDA.
DR   GO; GO:0005198; F:structural molecule activity; IC.
DR   GO; GO:0001525; P:angiogenesis; NAS.
DR   GO; GO:0016477; P:cell migration; IDA.
DR   GO; GO:0008283; P:cell proliferation; NAS.
DR   GO; GO:0008037; P:cell recognition; NAS.
DR   GO; GO:0007010; P:cytoskeleton organization and biogenesis; NAS.
DR   GO; GO:0009790; P:embryonic development; NAS.
DR   GO; GO:0045446; P:endothelial cell differentiation; NAS.
DR   GO; GO:0048041; P:focal adhesion formation; NAS.
DR   GO; GO:0007229; P:integrin-mediated signaling pathway; IMP.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR008211; Laminin_N.
DR   InterPro; IPR001638; SBP_bac_3.
DR   InterPro; IPR001368; TNFR_c6.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 20.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   Pfam; PF00055; Laminin_N; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   ProDom; PD003031; Laminin_B; 1.
DR   SMART; SM00180; EGF_Lam; 20.
DR   SMART; SM00281; LamB; 1.
DR   SMART; SM00282; LamG; 5.
DR   SMART; SM00136; LamNT; 1.
DR   PROSITE; PS00022; EGF_1; 19.
DR   PROSITE; PS01186; EGF_2; 3.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
DR   PROSITE; PS01039; SBP_BACTERIAL_3; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Laminin EGF-like domain; Signal.
FT   SIGNAL       1     35       Potential.
FT   CHAIN       36   3695       laminin alpha5 chain.
SQ   SEQUENCE   3695 AA;  399645 MW;  69703B52536EF0A3 CRC64;

  Query Match             23.2%;  Score 1042.5;  DB 2;  Length 3695;
  Best Local Similarity   31.6%;  Pred. No. 2.9e-60;
  Matches  294;  Conservative  159;  Mismatches  367;  Indels  109;  Gaps   32;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |:|||:|||::| | || ||  ||:|  :|| |:      |||| ||||:|:: |: ||:|
Db       2737 MKFNGRSGVQLRTPRDLADLAAYTALKFYLQGPEPEPGQGTEDRFVMYMGSRQATGDYMG 2796

Qy         61 MAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE--- 116
              ::: | ::  || || ||:    | : ||: : |           |   |  ||  :: | |
Db       2797 VSLRDKKVHWVYQLGEAGPAVLSIDEDIGEQ------FAAVSLDRTLQFGHMSVTVERQM 2850

Qy        117 --ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRPPPYKGCIEL 174
               |    ||    ||    |||| |:| ||||||||  |  |  |||| |:||||:
Db       2851 IQETKGDTVAPGA---EG-----LLNLRPDDFVFYVGGYPSTFTPPPLLRFPGYRGCIEM 2902

Qy        175 DDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPN-AP 228
              | ||| |:|||||: || |:|    || | |       :| :| :|||:|||       :
Db       2903 DTLNEEVVSLYNFERTFQLDTAVDRPCARSKSTGDPWLTDGSYLDGTGFARISFDSQIST 2962

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPP----- 275
              | | ::     |:||| : |  |: | :::|:|:: |   :         :||
Db       2963 TKRFEQELRLVSYSGVLFFLKQQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPPLTS 3022

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNER---SVRIEGEIFDFSTYYLGGI--- 329
              | |:           :  :|  :||: : |      ||  : ::     |||||:
Db       3023 ASKAIQ----------VFLLGGSRKRVLVRVERATVYSVEQDNDLELADAYYLGGVPPD 3071

Qy        330 --PIAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSR 384
               | ::|  |  :  : :||:| :|   |  : ||| | ||:  |: |  : |  :|
Db       3072 QLPPSLRWLFP-TGGSVRGCVKGIKALGKYVDLKRLN-TTGVSAGCTADLLVGRAMTFHG 3129

Qy        385 GG--QMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDS 442
              |  ::: :|:  | |       ||| : | |  |     :       |:|: | : |    :
Db       3130 HGFLRLALSNV-APLTGNVYSGFGFHSAQDSALLYYRASPDGLCQVSLQQGRVSLQLLRT 3188

Qy        443 NIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQV--LRRNQRLPSFSNAQQS----LR 496
              :   |:   : ||  |:|:  |: :|: | :|||:  :: ::  |      |    :
Db       3189 EV---KTQAGFADGAPHYVAFYSNATGVWLYVDDQLQQMKPHRGPPPELQPQPEGPPRLL 3245

Qy        497 LGG-------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFK 549
              |||        :| |||||| |||       | ||       : |  ||:    | |   :
Db       3246 LGGLPESGTIYNFSGCISNVFVQRLLGPQRVFDLQQNLGSVNVST-GCA----PALQA-Q 3299

Qy        550 SPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQFGDSPTSHLL 609
              :|    :|          |  | :|:| :       :|: | : :  : ||| | :||
Db       3300 TPGLGPRG-------LQATARKASRRSRQPARHPACMLPPHLRTTRDSYQFGGSLSSH-- 3350

Qy        610 LKLPQELLKPRS--QFSLDIQTTSPKGLVFYAG---TKDSFLALYVADGRVVFALGAGGK 664
              |:    | : |:    |: :  | :||: :          |||:::|  |   :  |
Db       3351 LEFVGILARHRNWPSLSMHVLPRSSRGLLLFTARLRPGSPSLALFLSNGHFVAQMEGLGT 3410

Qy        665 KLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRA--QEG---SLPGNSTISPREQVYL 719
              :|| :|::|   |:|| |       :  || || ||  |||      |      |
Db       3411 RLRAQSRQRSRPGRWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHQGAEHPQPHTLFVG 3470

Qy        720 GLPLSRKPKSLP-QHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGH 778
```

```
                ||| |     ||    | ||::  :|: :|| :|:   ||:||: | || |::|   ||
Db       3471 GLPASSHSSKLPVTVGFSGCVKRLRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGV 3530

Qy        779 VILANSVSLGPELKLTFSIRPRSLTGVLIHVG-SQSGQRLSVYMEAGKVTTSVSSDAGGS 837
                : |    :  |:: |   :|| ::||:: |:| :::   | : :   :|       ||
Db       3531 ITLDLPGATLPDVGLELEVRPLAVTGLIFHLGQARTPPYLQLQVTEKQVLLRADDGAGEF 3590

Qy        838 VTSITPKQSLCDGQWHSVAVSIKQRILHL 866
                ||:|    |||||| :||     :| |
Db       3591 STSVTRPSVLCDGQWHRLAVMKSGNVLRL 3619


RESULT 15
Q6ZQA1
ID   Q6ZQA1      PRELIMINARY;      PRT;  1524 AA.
AC   Q6ZQA1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MKIAA0533 protein (Fragment).
GN   Name=mKIAA0533;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryonic tail;
RX   PubMed=14621295;
RA   Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA   Saga Y., Nagase T., Ohara O., Koga H.;
RT   "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT   III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT   cDNAs identified by screening of terminal sequences of cDNA clones
RT   randomly sampled from size-fractionated libraries.";
RL   DNA Res. 10:167-180(2003).
DR   EMBL; AK129157; BAC97967.2; -.
DR   GO; GO:0005604; C:basement membrane; IDA.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005178; F:integrin binding; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0001763; P:branching morphogenesis; IDA.
DR   GO; GO:0030324; P:lung development; IMP.
DR   GO; GO:0007517; P:muscle development; IMP.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR001368; TNFR_c6.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00053; Laminin_EGF; 2.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   SMART; SM00180; EGF_Lam; 2.
DR   SMART; SM00282; LamG; 5.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_3.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
KW   Laminin EGF-like domain.
FT   NON_TER       1      1
FT   NON_TER    1524   1524
SQ   SEQUENCE   1524 AA;  166516 MW;  F43411828FF8E691 CRC64;

  Query Match             21.2%;  Score 950;  DB 2;  Length 1524;
  Best Local Similarity   30.6%;  Pred. No. 1.3e-54;
  Matches  285;  Conservative  167;  Mismatches  360;  Indels  120;  Gaps   37;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGG--TEDMFVMYLGNKDASKDY 58
              |:|||:||| :| | || ||  ||:|   :| |       |  | | ||:|:|:: |: ||
Db        572 MKFNGRSGVRLRTPRDLADLAAYTALKFHIQSPVPAPEPGKNTGDHFVLYMGSRQATGDY 631

Qy         59 IGMAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEA 117
              :|::: : ::  || ||       : ||: : |           |   |  ||  :: | |
Db        632 MGVSLRNQKVHWVYRLGKAGPTTLSIDENIGEQ------FAAVSIDRTLQFGHMSVTVE- 684

Qy        118 TSNKPKAPAVYDLEGGS----SNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIE 173
                        |::::| :    |  |||| |:| |||||||| :|  |  |||| | ||||
Db        685 ------KQMVHEIKGDTVAPGSEGLLNLHPDDFVFYVGGYPSNFTPPEPLRFPGYLGCIE 738

Qy        174 LDDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPNAP 228
              :: ||| |:|||||: || |:|   :|| | |       :| :| :|:|:|||  :
Db        739 METLNEEVVSLYNFEQTFMLDTAVDKPCARSKATGDPWLTDGSYLDGSGFARISFEKQ-- 796

Qy        229 FPN---FIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPPK- 276
              | |   | | ::      |::|| : :  |: | :::| |:: |    |         :||:
Db        797 FSNTKRFDQELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFGSGLKKADPLQPPQA 856

Qy        277 ----EKGIRDTINDGKDHSILITIGKLQKRMWINVNERSVRIEGEIFDFSTYYLGGI--- 329
                  | |:  :  |    :|:   ::::    :|:: ::    |: |   |||||:
Db        857 LTAASKAIQVFLLAGNRKRVLV---RVERATVFSVDQDNML---EMAD--AYYLGGVPPE 908

Qy        330 --PIAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSR 384
                |:::|: |  |  : :|||:| :|    |   : ||| | |::  |: |  : || :|
Db        909 QLPLSLRQLFP-SGGSVRGCIKGIKALGKYVDLKRLN-TTGISFGCTADLLVGRTMTFHG 966

Qy        385 GGQMSFTNLDV-PSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSN 443
              | :     || | |:     |||:  | :  |    :       |:| :||:  |   :
Db        967 HGFLPLALPDVAPITEVVYSGFGFRGTQDNNLLYYRTSPDGPYQVSLREGHVTLRFMNQE 1026

Qy        444 IPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDD--QVLRRNQRLPSFSNAQ----QSLRL 497
              :   ::   : ||  |:|:  |: :|: | :||  |::: ::|       |      | |
Db       1027 V---ETQRVFADGAPHYVAFYSNVTGVWLYVDDQLQLVKSHERTTPMLQLQPEEPSRLLL 1083

Qy        498 GG-------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKS 550
              ||        :| |||||| |||     | ||       : |: ||:    |  ::  |
Db       1084 GGLPVSGTFHNFSGCISNVFVQRLRGPQRVFDLHQNMGSVNVSV-GCT----PAQLIETS 1138

Qy        551 PKRFNKGRIFNVNQLMQDAPQATRSTEAW-----QDGRSCLPPLNTKASHRALQF-GDSP 604
                    |     |::  :   |    | |     ||       || :      ||| | ||
Db       1139 RATAQK-----VSRRSRQPSQDLACTTPWLPGTIQDAYQFGGPLPS-----YLQFVGISP 1188

Qy        605 TSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALGAGGK 664
              :    | |  |::| :     : :|:|      :|   | | |::   |  |       |
Db       1189 SHRNRLHLSM-LVRPHAASQGLLLSTAP-----MSGRSPS-LVLFLNHGHFVAQTEGPGP 1241

Qy        665 KLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRA-QEGSLPGNSTISPREQVYL---- 719
              :|:::|::    |:|| |       : :|||| :   : :|      : | | |
Db       1242 RLQVQSRQHSRAGQWHRVSVRWGMQQIQLVVDGSQTWSQKALHHRVPRAERPQPYTLSVG 1301

Qy        720 GLPLSRKPKSLP-QHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGH 778
              ||| |     ||    | |||:  ||: :|| :|:   ||:||: | || |::|    |
Db       1302 GLPASSYSSKLPVSVGFSGCLKKLQLDKQPLRTPTQMVGVTPCVSGPLEDGLFFPGSEGV 1361

Qy        779 VILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSV-YMEAGKVTTSV---SSDA 834
              | |   :  | : |   :|| :  |:: |:    || |:  ||:   :|  |   ::|
Db       1362 VTLELPKAKMPYVSLELEMRPLAAAGLIFHL----GQALATPYMQLKVLTEQVLLQANDG 1417

Qy        835 GGSVTSITPKQSLCDGQWHSVAVSIKQRILHL 866
              |  ::      ||||:|| ||| : :  | |
Db       1418 AGEFSTWVTYPKLCDGRWHRVAVIMGRDTLRL 1449


Search completed: February 22, 2005, 08:24:20
Job time : 151.522 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:04:10 ; Search time 159.651 Seconds
(without alignments)
2097.921 Million cell updates/sec

Title: US-10-817-423-2
Perfect score: 4491
Sequence: 1 MRFNGKSGVEVRLPNDLEDL.....LCDGQWHSVAVSIKQRILHL 866

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4491	100.0	1694	3	AAB48461	Aab48461 Rat lamin
2	4491	100.0	1725	3	AAB48460	Aab48460 Rat lamin
3	3560.5	79.3	1693	3	AAB48459	Aab48459 Human lam
4	3560.5	79.3	1693	3	AAB48457	Aab48457 Human lam
5	3560.5	79.3	1713	3	AAB48458	Aab48458 Human lam
6	3560.5	79.3	1713	6	ABR92102	Abr92102 Human cer
7	3560.5	79.3	1713	7	ADD29904	Add29904 Human lam
8	3560.5	79.3	1713	7	ADG37225	Adg37225 Human lam
9	3560.5	79.3	1713	8	ABM81957	Abm81957 Tumour-as
10	3560.5	79.3	1713	8	ADR87606	Adr87606 Human Lam
11	3560.5	79.3	1724	3	AAB48456	Aab48456 Human lam
12	3560.5	79.3	3332	7	ADE08094	Ade08094 Novel pro
13	3552.5	79.1	1713	2	AAR70148	Aar70148 Deduced s
14	1599	35.6	469	4	AAG75103	Aag75103 Human col
15	1310	29.2	770	2	AAW26584	Aaw26584 Rat hemid
16	1198	26.7	1792	3	AAB48443	Aab48443 Human lam
17	1198	26.7	1800	3	AAB48445	Aab48445 Human lam
18	1198	26.7	1816	3	AAB48442	Aab48442 Human lam
19	1198	26.7	1816	8	ADR87600	Adr87600 Human Lam
20	1198	26.7	1824	3	AAB48444	Aab48444 Human lam
21	1192	26.5	1823	5	ABP63020	Abp63020 Human pol
22	1190	26.5	1581	7	ADJ68348	Adj68348 Human hea
23	1190	26.5	1816	8	ADP08401	Adp08401 Human lam
24	1187	26.4	984	5	ABB80819	Abb80819 Heparin b
25	1187	26.4	1816	7	ADC01877	Adc01877 Human lam
26	1185	26.4	1816	7	ADC01879	Adc01879 Human lam
27	1183	26.3	1792	3	AAB48447	Aab48447 Mouse lam
28	1183	26.3	1816	3	AAB48446	Aab48446 Mouse lam
29	1181.5	26.3	1815	5	ABB80853	Abb80853 Heparin b
30	1170.5	26.1	983	5	ABB80818	Abb80818 Heparin b
31	1045.5	23.3	1677	8	ADM87708	Adm87708 Human EST
32	1045.5	23.3	3695	5	ADI28030	Adi28030 ECMCAD pr
33	1045.5	23.3	3695	8	ADN04478	Adn04478 Antipsori
34	1045.5	23.3	3696	5	AAE17310	Aae17310 Human lam
35	1045.5	23.3	3705	5	AAE17309	Aae17309 Human lam
36	1042.5	23.2	1601	4	AAM39009	Aam39009 Human pol
37	1042.5	23.2	1645	7	ADL15098	Adl15098 Human mal
38	1042.5	23.2	1645	7	ADN95658	Adn95658 Human BEC
39	1042.5	23.2	3695	5	ABB81588	Abb81588 Human lam
40	1042	23.2	1640	5	ABB09504	Abb09504 Human lam
41	1042	23.2	1640	8	ADO10049	Ado10049 Novel hum
42	1041	23.2	3690	8	ADM87254	Adm87254 Human pro
43	1015.5	22.6	953	5	AAM50358	Aam50358 Human lam
44	948	21.1	3635	5	ABB81589	Abb81589 Mouse lam
45	948	21.1	3635	5	AAM50357	Aam50357 Mouse lam

ALIGNMENTS

RESULT 1
AAB48461
ID AAB48461 standard; protein; 1694 AA.
XX
AC AAB48461;
XX
DT 02-MAR-2001 (first entry)
XX
DE Rat laminin 5 polypeptide, SEQ ID NO: 12.
XX
KW Rat; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS Rattus norvegicus.
XX
PN WO200066731-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011459.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (BIOS-) BIOSTATUM INC.
XX
PI Boutaud A;
XX
DR WPI; 2000-687538/67.
DR N-PSDB; AAC83722.
XX
PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burns, acute wounds and skin grafts.
XX
PS Claim 3; Page 117-122; 232pp; English.
XX
CC The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of Type
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotrimeric laminin, whereas

```
CC   prior art cell lines have been created that produce but do not secreted
CC   only one or two chain laminins
XX
SQ   Sequence 1694 AA;

  Query Match           100.0%;  Score 4491;  DB 3;  Length 1694;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  866;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 810

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 870

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 930

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 990

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 1050

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 1110

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 1170

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 1230

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 1290

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQF 1350

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALG 1410

Qy        661 AGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYLG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1411 AGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYLG 1470

Qy        721 LPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1471 LPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHVI 1530

Qy        781 LANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTS 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1531 LANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTS 1590

Qy        841 ITPKQSLCDGQWHSVAVSIKQRILHL 866
              ||||||||||||||||||||||||||
Db       1591 ITPKQSLCDGQWHSVAVSIKQRILHL 1616


RESULT 2
AAB48460
ID   AAB48460 standard; protein; 1725 AA.
XX
AC   AAB48460;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Rat laminin 5 polypeptide, SEQ ID NO: 10.
XX
KW   Rat; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW   cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW   periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS   Rattus norvegicus.
XX
PN   WO200066731-A2.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011459.
XX
PR   30-APR-1999;   99US-0131720P.
PR   21-AUG-1999;   99US-0149738P.
PR   24-SEP-1999;   99US-0155945P.
XX
PA   (BIOS-) BIOSTATUM INC.
XX
PI   Boutaud A;
XX
DR   WPI; 2000-687538/67.
DR   N-PSDB; AAC83721.
XX
PT   Laminin 5-expressing cells, used to accelerate wound healing associated
PT   with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT   burns, acute wounds and skin grafts.
XX
PS   Claim 3; Page 104-109; 232pp; English.
XX
CC   The present sequence is a laminin 5 chain polypeptide. Recombinant
CC   laminin 5-expressing cells are used to accelerate wound healing,
CC   especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC   surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC   intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC   improve the biocompatibility of medical devices, and to promote cell
CC   adhesion to a surface. They can be used for the ex vivo treatment of Type
CC   I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC   line produces and secretes recombinant heterotrimeric laminin, whereas
CC   prior art cell lines have been created that produce but do not secreted
CC   only one or two chain laminins
XX
SQ   Sequence 1725 AA;

  Query Match           100.0%;  Score 4491;  DB 3;  Length 1725;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  866;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 841

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 901

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 961

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 1021

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 1081
```

```
Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 1141

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 1201

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 1261

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 1321

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQF 1381

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALG 1441

Qy        661 AGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYLG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 AGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYLG 1501

Qy        721 LPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1502 LPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHVI 1561

Qy        781 LANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTS 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 LANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTS 1621

Qy        841 ITPKQSLCDGQWHSVAVSIKQRILHL 866
              ||||||||||||||||||||||||||
Db       1622 ITPKQSLCDGQWHSVAVSIKQRILHL 1647
```

RESULT 3
AAB48459
ID AAB48459 standard; protein; 1693 AA.
XX
AC AAB48459;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human laminin 5 polypeptide, SEQ ID NO: 8.
XX
KW Human; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS Homo sapiens.
XX
PN WO200066731-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011459.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (BIOS-) BIOSTATUM INC.
XX
PI Boutaud A;
XX
DR WPI; 2000-687538/67.
DR N-PSDB; AAC83720.
XX
PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burns, acute wounds and skin grafts.
XX
PS Claim 3; Page 91-97; 232pp; English.
XX
CC The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of Type
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotrimeric laminin, whereas
CC prior art cell lines have been created that produce but do not secreted
CC only one or two chain laminins
XX
SQ Sequence 1693 AA;

Query Match 79.3%; Score 3560.5; DB 3; Length 1693;
Best Local Similarity 78.4%; Pred. No. 2.9e-307;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||: |||||||:|||||||||||||:||||
Db        751 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 810

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||:|:||:||::|||||||||||||||:||||| |||:
Db        811 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 870

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: |||||||||||:||||| ||||||||||||||||
Db        871 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 930

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| |||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        931 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 990

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db        991 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1050

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||||:|||||||||||||||
Db       1051 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1110

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||:|||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1111 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1170

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1171 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1230

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ::||   |:::|||||||| :||||||| ||| | ||||||| | | |:| ||||||||
Db       1231 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1290

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |    |:|:| |||
Db       1291 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1348

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| |||||||||||::|:|||| :|||: |||:||:|||:: ||:||||
Db       1349 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1408

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       1409 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRARAGSLPGNSTISIRAPVYL 1468
```

```
Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :||||||::|||:|||| :||: |||| |||| |||||||||: ||||
Db       1469 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1528

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || ||||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1529 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1588

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:||||||||||||||||:||| ||||
Db       1589 SVTPKQSLCDGQWHSVAVTIKQHILHL 1615


RESULT 4
AAB48457
ID   AAB48457 standard; protein; 1693 AA.
XX
AC   AAB48457;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human laminin 5 polypeptide, SEQ ID NO: 4.
XX
KW   Human; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW   cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW   periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS   Homo sapiens.
XX
PN   WO200066731-A2.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011459.
XX
PR   30-APR-1999;   99US-0131720P.
PR   21-AUG-1999;   99US-0149738P.
PR   24-SEP-1999;   99US-0155945P.
XX
PA   (BIOS-) BIOSTATUM INC.
XX
PI   Boutaud A;
XX
DR   WPI; 2000-687538/67.
DR   N-PSDB; AAC83718.
XX
PT   Laminin 5-expressing cells, used to accelerate wound healing associated
PT   with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT   burns, acute wounds and skin grafts.
XX
PS   Claim 3; Page 66-71; 232pp; English.
XX
CC   The present sequence is a laminin 5 chain polypeptide. Recombinant
CC   laminin 5-expressing cells are used to accelerate wound healing,
CC   especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC   surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC   intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC   improve the biocompatibility of medical devices, and to promote cell
CC   adhesion to a surface. They can be used for the ex vivo treatment of Type
CC   I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC   line produces and secretes recombinant heterotrimeric laminin, whereas
CC   prior art cell lines have been created that produce but do not secreted
CC   only one or two chain laminins
XX
SQ   Sequence 1693 AA;

  Query Match             79.3%;  Score 3560.5;  DB 3;  Length 1693;
  Best Local Similarity   78.4%;  Pred. No. 2.9e-307;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||: |||||||:|||||||||||||:||||

Db        751 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 810

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||::|||||||||||||:||||| |||:
Db        811 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 870

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:|||| |||||||||||||||||
Db        871 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 930

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| |||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        931 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 990

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||| |||:|: | ||:|:|||| | |||||
Db        991 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1050

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||:|||||||||||||||||
Db       1051 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1110

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||:|||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1111 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1170

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:|||||  ||  |||||| |||||||:|||||| |||||||||:||
Db       1171 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1230

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ::||   |:::|||||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1231 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1290

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1291 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1348

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| |||||||||||::|:|||| :||||: |||:||:|||:: ||:||||
Db       1349 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1408

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       1409 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 1468

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :||||||::|||:|||| :||: |||| |||| |||||||||: ||||
Db       1469 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1528

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || ||||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1529 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1588

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:||||||||||||||||:||| ||||
Db       1589 SVTPKQSLCDGQWHSVAVTIKQHILHL 1615


RESULT 5
AAB48458
ID   AAB48458 standard; protein; 1713 AA.
XX
AC   AAB48458;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human laminin 5 polypeptide, SEQ ID NO: 6.
XX
KW   Human; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW   cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW   periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
```

OS Homo sapiens.
XX
PN WO200066731-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011459.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (BIOS-) BIOSTATUM INC.
XX
PI Boutaud A;
XX
DR WPI; 2000-687538/67.
DR N-PSDB; AAC83719.
XX
PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burns, acute wounds and skin grafts.
XX
PS Claim 3; Page 79-84; 232pp; English.
XX
CC The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of Type
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotrimeric laminin, whereas
CC prior art cell lines have been created that produce but do not secreted
CC only one or two chain laminins
XX
SQ Sequence 1713 AA;

Query Match 79.3%; Score 3560.5; DB 3; Length 1713;
Best Local Similarity 78.4%; Pred. No. 2.9e-307;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              |||||||||||||||||||:|:||:||:||::||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :||||||||||: ||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||||||:||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
```

```
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1368

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| ||||||||||||::|:|||| :|||: |||:||:|||:: ||:||||
Db       1369 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1428

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       1429 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 1488

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :||||||::|||:|||| :||: |||| |||| |||||||: ||||
Db       1489 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1548

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || ||||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1549 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1608

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:|||||||||||||||:||| ||||
Db       1609 SVTPKQSLCDGQWHSVAVTIKQHILHL 1635
```

RESULT 6
ABR92102
ID ABR92102 standard; protein; 1713 AA.
XX
AC ABR92102;
XX
DT 10-SEP-2003 (first entry)
XX
DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:113.
XX
KW Human; cervical cancer; cervical cancer marker; cancer therapy;
KW detection; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO2002101075-A2.
XX
PD 19-DEC-2002.
XX
PF 12-JUN-2002; 2002WO-US018638.
XX
PR 13-JUN-2001; 2001US-0298155P.
PR 13-JUN-2001; 2001US-0298159P.
PR 14-NOV-2001; 2001US-0335936P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Schlegel R, Chen Y, Zhao X, Monahan JE, Kamatkar S;
PI Gannavarapu M, Glatt K, Hoersch S;
XX
DR WPI; 2003-156967/15.
DR N-PSDB; ACF12884.
XX
PT New isolated nucleic acid molecule useful for detecting, characterizing,
PT preventing and treating human cervical cancers, in various prognostic and
PT diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
XX
PS Claim 4; Page 269-273; 386pp; English.
XX
CC ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)
CC given in ABR92047 to ABR92164. A higher level of expression of (I) than
CC normal indicates the presence of cervical cancer. Also described: (1) a

CC vector (II) containing (I); (2) a host cell (III) containing (I); and (3)
CC assessing (M1) whether a patient is afflicted with cervical cancer,
CC comprising comparing the level of expression of a marker in a patient's
CC sample, and the normal level of expression of the marker in a control non
CC -cervical cancer sample, where a significant increase in the level of
CC expression of the marker in the patient's sample relative to that in the
CC control sample is an indication that the patient is afflicted with
CC cervical cancer. (I) has cytostatic activity, and can be used in gene
CC therapy and in vaccines. (I) is useful in detecting, characterising,
CC preventing and treating human cervical cancers. (I) may also be used in
CC various prognostic and diagnostic assays, pharmacogenomics and in
CC monitoring clinical trials
XX
SQ Sequence 1713 AA;

Query Match 79.3%; Score 3560.5; DB 6; Length 1713;
Best Local Similarity 78.4%; Pred. No. 2.9e-307;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||:|||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| |||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1368

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| ||||||||||||::|:|||| :|||: |||:||:|||:: ||:||||
Db       1369 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1428

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       1429 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRARAEGSLPGNSTISIRAPVYL 1488

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :|||||::|||:|||| :||: |||| |||| ||||||||: ||||
Db       1489 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1548

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || ||||||||||:|||:||| |: | ||:|||||| |: | |||: |
```

Db 1549 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1608

Qy 840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
|:||||||||||||||||:||| ||||
Db 1609 SVTPKQSLCDGQWHSVAVTIKQHILHL 1635

RESULT 7
ADD29904
ID ADD29904 standard; protein; 1713 AA.
XX
AC ADD29904;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human laminin alpha 3 seq id 2.
XX
KW ophthalmological; dermatological; laminin alpha 3; G3 domain;
KW cell adhesion function; cell movement effect; epithelial tissue function;
KW retinal detachment; cosmetic surgery; skin graft; human.
XX
OS Homo sapiens.
XX
PN JP2003093064-A.
XX
PD 02-APR-2003.
XX
PF 20-SEP-2001; 2001JP-00287519.
XX
PR 20-SEP-2001; 2001JP-00287519.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (KIHA-) ZH KIHARA KINEN YOKOHAMA SEIMEI KAGAKU.
XX
DR WPI; 2003-817304/77.
DR N-PSDB; ADD29903.
XX
PT Novel modified G3 domain of laminin alpha 3 chain useful for controlling
PT cell adhesion and cell movement.
XX
PS Claim 1; SEQ ID NO 2; 49pp; Japanese.
XX
CC The invention describes a modified laminin alpha3 chain comprising one or
CC more amino acid deletions, substitutions or additions at region
CC corresponding to a region of G3 domain having amino acids 1214-1324 of
CC laminin alpha3 chain having a fully defined sequence of 1713 amino acids
CC as given in the specification. (I) can control cell adhesion function and
CC cell movement effect. A composition comprising laminin is useful for
CC maintaining or treating the function of epithelial tissue and for
CC treatment or prevention of retinal detachment and in cosmetic surgery and
CC skin graft. The modified region of laminin alpha3 chain can control cell
CC adhesion function and cell movement effect. This is the amino acid
CC sequence of human laminin alpha 3.
XX
SQ Sequence 1713 AA;

Query Match 79.3%; Score 3560.5; DB 7; Length 1713;
Best Local Similarity 78.4%; Pred. No. 2.9e-307;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
```

```
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||||:|||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ::||   |:::||||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1368

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| ||||||||||||::|:|||| :|||| :|||:||:|||:: ||:||||
Db       1369 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1428

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       1429 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 1488

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :||||||::|||:|||| :||: |||| |||| ||||||||: ||||
Db       1489 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1548

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || |||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1549 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1608

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:|||||||||||||:||| ||||
Db       1609 SVTPKQSLCDGQWHSVAVTIKQHILHL 1635


RESULT 8
ADG37225
ID   ADG37225 standard; protein; 1713 AA.
XX
AC   ADG37225;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human laminin-6 alpha 3 subunit.
XX
KW   human; laminin-6; alpha 3; B1 subunit; B2 subunit; cell-movement;
KW   cell-adhesion; dermatological; neuroprotective; muscular;
KW   epithelial tissue; nervous tissue; varicella disease.
XX
OS   Homo sapiens.
XX
PN   JP2003212791-A.
XX
PD   30-JUL-2003.
XX
PF   17-JAN-2002; 2002JP-00009227.
XX
PR   17-JAN-2002; 2002JP-00009227.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2003-819867/77.
DR   N-PSDB; ADG37224.
XX
PT   Composition comprising laminin-6 for regulation of cell-movement activity
PT   and/or cell-adhesion activity, useful for treating or maintaining
PT   function of epithelial tissue, nervous tissue and muscles.
XX
PS   Claim 2; SEQ ID NO 2; 55pp; Japanese.
XX
CC   This invention describes a novel composition comprising the human laminin
CC   -6 alpha 3, B1 or B2 subunits for regulation of cell-movement activity
CC   and/or cell-adhesion activity. The products of the invention have
CC   dermatological, neuroprotective and muscular activity. The composition of
CC   the invention is useful for treating or maintaining the function of the
CC   epithelial tissue, the nervous tissue and muscles and is also useful for
CC   treatment or prevention of varicella disease.
XX
SQ   Sequence 1713 AA;

  Query Match             79.3%;  Score 3560.5;  DB 7;  Length 1713;
  Best Local Similarity   78.4%;  Pred. No. 2.9e-307;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||||||||: |||||||:||||||||||:|||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||::||:|||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :||||||||||: ||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||| ||||||||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||||:|||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ::||   |:::||||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1368

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| ||||||||||||::|:|||| :|||| :|||:||:|||:: ||:||||
Db       1369 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1428

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       1429 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 1488

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
```

```
                | | | |||||| :||||||::|||:|||| :||: |||| |||| ||||||||: ||||
Db       1489 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1548

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || ||||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1549 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1608

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:||||||||||||||||:||| ||||
Db       1609 SVTPKQSLCDGQWHSVAVTIKQHILHL 1635


RESULT 9
ABM81957
ID   ABM81957 standard; protein; 1713 AA.
XX
AC   ABM81957;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Tumour-associated antigenic target (TAT) polypeptide PRO2799, SEQ:5041.
XX
KW   Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW   tumour; diagnosis; cell proliferative disorder; breast cancer;
KW   colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW   central nervous system cancer; bladder cancer; pancreatic cancer;
KW   cervical cancer; melanoma; leukaemia; hybridisation probe;
KW   chromosome identification; chromosome mapping; gene mapping;
KW   gene therapy; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2004030615-A2.
XX
PD   15-APR-2004.
XX
PF   29-SEP-2003; 2003WO-US028547.
XX
PR   02-OCT-2002; 2002US-0414971P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Wu TD,  Zhang Z,  Zhou Y;
XX
DR   WPI; 2004-347921/32.
DR   N-PSDB; ACN40327.
XX
PT   New tumor-associated antigenic target polypeptides and nucleic acids,
PT   useful in preparing a medicament for treating or detecting a
PT   proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT   prostate cancer or tumor.
XX
PS   Claim 12; SEQ ID NO 5041; 7273pp; English.
XX
CC   The invention relates to human tumour-associated antigenic target (TAT)
CC   polypeptides, and their related nucleic acids. The TAT polypeptides are
CC   overexpressed in cancer tissues compared to normal tissues, and may thus
CC   serve as effective targets for the diagnosis and treatment of cancer in
CC   mammals. The invention also relates to nucleic acid and polypeptide
CC   sequences at least 80% identical to the TAT nucleic acids and
CC   polypeptides; expression vectors and host cells comprising a TAT nucleic
CC   acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC   molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC   TAT polypeptide; and methods and compositions for the treatment or
CC   diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC   antibodies, antagonists, binding molecules and compositions are useful
CC   for diagnosing or treating a cell proliferative disorder associated with
CC   increased TAT expression, particularly cancers such as breast cancer,
CC   colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC   cancer, pancreatic cancer, cervical cancer, cancers of the central
CC   nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC   used as hybridisation probes, in chromosome and gene mapping, in
CC   chromosome identification and in gene therapy. The present sequence
CC   represents a TAT polypeptide of the invention
XX
SQ   Sequence 1713 AA;

  Query Match             79.3%;  Score 3560.5;  DB 8;  Length 1713;
  Best Local Similarity   78.4%;  Pred. No. 2.9e-307;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||: |||||||:|||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| |||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| |||||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||:|||||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| |||||||:||||| ||  |||||| |||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1368

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| |||||||||||||::|:|||| :||||: |||:||:|||:: ||:||||
Db       1369 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1428

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       1429 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 1488

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :||||||::|||:|||| :||: |||| |||| ||||||||: ||||
Db       1489 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1548

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || ||||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1549 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1608

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:||||||||||||||||:||| ||||
Db       1609 SVTPKQSLCDGQWHSVAVTIKQHILHL 1635


RESULT 10
ADR87606
ID   ADR87606 standard; protein; 1713 AA.
XX
```

```
AC   ADR87606;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Human Laminin alpha 3 (nicein), SEQ ID 10.
XX
KW   Cytostatic; Gene Therapy; renal cell carcinoma; Wilms tumour; human;
KW   Laminin alpha 3; nicein.
XX
OS   Homo sapiens.
XX
PN   WO2004075835-A2.
XX
PD   10-SEP-2004.
XX
PF   20-FEB-2004; 2004WO-US005042.
XX
PR   21-FEB-2003; 2003US-00372683.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Gerritsen ME,  Peale FV,  Wu TD;
XX
DR   WPI; 2004-676901/66.
DR   N-PSDB; ADR87605.
XX
PT   New anti-EDNRA antibody, useful in preparing a composition for diagnosing
PT   or inhibiting the growth of renal cell carcinoma or Wilms tumor.
XX
PS   Example 1; SEQ ID NO 10; 257pp; English.
XX
CC   The present invention relates to novel antibodies which bind to proteins
CC   which are overexpressed in renal cell carcinomas or Wilms tumour. The
CC   antibody can bind to a protein comprising CXCR4 (ADR87598), Laminin alpha
CC   4 (ADR87600), TIMP1 (ADR87602), Type IV collagen alpha 1 (ADR87604),
CC   Laminin alpha 3 (nicein) (ADR87606), Adrenomedullin (ADR87608), Type IV
CC   collagen alpha 2 (ADR87610), Thrombospondin 2 (ADR87612), Type I collagen
CC   alpha 2 (ADR87614), Type VI collagen alpha 3 (ADR87616), Latent TGFbeta
CC   binding protein 2 (LTBP2) (ADR87618), Serine or cystein protease
CC   inhibitor heat shock protein 47 (HSP47) (ADR87620), Procollagen-lysine, 2
CC   -oxoglutarate 5-dioxygenase (ADR87622), connexin 43 (ADR87624), Type IV
CC   collagen alpha 2 (ADR87626), Connexin 37 (ADR87628), Ephrin A1
CC   (ADR87630), Laminin beta 2 (ADR87632), Integrin alpha 1, hevin
CC   (ADR87635), Stanniocalcin 1 (ADR87637), Thrombospondin 4 (ADR87639), CD36
CC   polypeptide (ADR87641), Endothelin receptor A (EDNRA, ADR87643) or
CC   Endothelin receptor B (EDNRB ADR87645). The proteins of ADR87598-ADR87641
CC   and ADR87645 are all overexpressed in renal call carcinoma, and ADR87643
CC   (EDNRA) is overexpressed in Wilms tumour. The antibodies are useful in
CC   preparing a composition for diagnosing or inhibiting the growth of renal
CC   cell carcinoma or Wilms tumour. The present sequence is one such protein
CC   of the invention.
XX
SQ   Sequence 1713 AA;

  Query Match             79.3%;  Score 3560.5;  DB 8;  Length 1713;
  Best Local Similarity   78.4%;  Pred. No. 2.9e-307;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||: |||||||:|||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:|||||  |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:|||||  ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||||:|||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1368

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| ||||||||||||::|:|||| :|||: |||:||:|||:: ||:||||
Db       1369 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1428

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||||| |  |||
Db       1429 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRARERGSLPGNSTISIRAPVYL 1488

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :|||||::|||:|||| :||: |||| |||| |||||||||: ||||
Db       1489 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1548

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || ||||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1549 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1608

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:|||||||||||||||:||| ||||
Db       1609 SVTPKQSLCDGQWHSVAVTIKQHILHL 1635


RESULT 11
AAB48456
ID   AAB48456 standard; protein; 1724 AA.
XX
AC   AAB48456;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human laminin 5 polypeptide, SEQ ID NO: 2.
XX
KW   Human; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW   cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW   periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS   Homo sapiens.
XX
PN   WO200066731-A2.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011459.
XX
PR   30-APR-1999;   99US-0131720P.
PR   21-AUG-1999;   99US-0149738P.
PR   24-SEP-1999;   99US-0155945P.
XX
PA   (BIOS-) BIOSTATUM INC.
```

```
XX
PI   Boutaud A;
XX
DR   WPI; 2000-687538/67.
DR   N-PSDB; AAC83717.
XX
PT   Laminin 5-expressing cells, used to accelerate wound healing associated
PT   with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT   burns, acute wounds and skin grafts.
XX
PS   Claim 3; Page 53-59; 232pp; English.
XX
CC   The present sequence is a laminin 5 chain polypeptide. Recombinant
CC   laminin 5-expressing cells are used to accelerate wound healing,
CC   especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC   surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC   intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC   improve the biocompatibility of medical devices, and to promote cell
CC   adhesion to a surface. They can be used for the ex vivo treatment of Type
CC   I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC   line produces and secretes recombinant heterotrimeric laminin, whereas
CC   prior art cell lines have been created that produce but do not secreted
CC   only one or two chain laminins
XX
SQ   Sequence 1724 AA;

  Query Match             79.3%;  Score 3560.5;  DB 3;  Length 1724;
  Best Local Similarity   78.4%;  Pred. No. 3e-307;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        782 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 841

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        842 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 901

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:|||| |||||||||||||||
Db        902 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 961

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        962 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1021

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||| |||:|: | ||:|:|||| | |||||
Db       1022 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1081

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||:|||||||||||||||
Db       1082 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1141

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | |||||||||| ||:||
Db       1142 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1201

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| |||||||:|||||| ||||||||||:||
Db       1202 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1261

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | |||||| | | |:| ||||||||
Db       1262 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1321

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1322 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1379

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| |||||||||||||::|:|||| :||||: |||:||:|||:: ||:||||
Db       1380 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1439

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       1440 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 1499

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :||||||::|||:|||| :||: |||| |||| |||||||: ||||
Db       1500 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1559

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || |||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1560 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1619

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:|||||||||||||||:||| ||||
Db       1620 SVTPKQSLCDGQWHSVAVTIKQHILHL 1646


RESULT 12
ADE08094
ID   ADE08094 standard; protein; 3332 AA.
XX
AC   ADE08094;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Novel protein (useful for identifying genetic disorders) #249.
XX
KW   novel gene; novel protein; tissue marker; molecular weight marker;
KW   chromosome marker; genetic disorder.
XX
OS   Unidentified.
XX
PN   WO2003054152-A2.
XX
PD   03-JUL-2003.
XX
PF   10-DEC-2002; 2002WO-US039555.
XX
PR   10-DEC-2001; 2001US-0339739P.
PR   11-DEC-2001; 2001US-0339453P.
PR   14-MAR-2002; 2002US-0365091P.
PR   14-MAR-2002; 2002US-0365384P.
PR   12-APR-2002; 2002US-0372381P.
PR   12-APR-2002; 2002US-0372615P.
PR   22-APR-2002; 2002US-00128558.
PR   24-APR-2002; 2002US-0376045P.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI   Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI   Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
DR   WPI; 2003-569235/53.
DR   N-PSDB; ADE07183.
XX
PT   New polynucleotides, useful for expressing recombinant proteins for
PT   analysis, characterization or therapeutic use, or as markers for tissues
PT   in which the corresponding protein is preferentially expressed.
XX
PS   Claim 20; SEQ ID NO 1160; 1177pp; English.
XX
CC   The invention comprises the amino acid and coding sequences of novel
CC   proteins. The DNA and protein sequences of the invention are useful as:
CC   markers for tissues in which the corresponding protein is preferentially
CC   expressed; as molecular weight markers on gels; as chromosome markers or
CC   tags; to identify chromosomes or to map related gene positions; and to
CC   compare with endogenous DNA sequences in patients to identify potential
CC   genetic disorders. The present amino acid sequence represents a protein
CC   of the invention.
XX
SQ   Sequence 3332 AA;
```

Query Match 79.3%; Score 3560.5; DB 7; Length 3332;
Best Local Similarity 78.4%; Pred. No. 8.8e-307;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||||||: ||||||||:||||||||||||:||||
Db       2390 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 2449

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db       2450 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 2509

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :||||||||||: ||||||||||:||||| ||||||||||||||||
Db       2510 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 2569

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| |||||||||||||||||||||||||||||:||||:|| | | |||||||
Db       2570 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 2629

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       2630 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 2689

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||:||||||||||||||||
Db       2690 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 2749

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       2750 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 2809

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       2810 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 2869

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| |||||||||
Db       2870 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 2929

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       2930 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 2987

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| ||||||||||||::|:|||| :|||: |||:||:|||:: ||:||||
Db       2988 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 3047

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||:|||||||||| | |||
Db       3048 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 3107

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :||||||::|||:|||| :||: |||| |||| ||||||||: ||||
Db       3108 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 3167

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || |||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       3168 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 3227

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:|||||||||||||||:||| ||||
Db       3228 SVTPKQSLCDGQWHSVAVTIKQHILHL 3254
```

RESULT 13
AAR70148
ID AAR70148 standard; protein; 1713 AA.
XX
AC AAR70148;
XX
DT 25-MAR-2003 (revised)
DT 05-OCT-1995 (first entry)
XX
DE Deduced sequence of cDNA corresp. to the alpha-3EpA transcript.
XX
KW E170; epithelial ligand glycoprotein; epiligrin complex;
KW epithelial cell binding.
XX
OS Homo sapiens.
XX
PN WO9506660-A1.
XX
PD 09-MAR-1995.
XX
PF 02-SEP-1994; 94WO-US010261.
XX
PR 02-SEP-1993; 93US-00115918.
XX
PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
XX
PI Carter WG, Gil SG, Ryan MC;
XX
DR WPI; 1995-115398/15.
DR N-PSDB; AAQ83236.
XX
PT New nucleic acid encoding epiligrin, an epithelial ligand complex - also
PT related vectors, transformed cells, proteins and antibodies, useful
PT therapeutically and diagnostically, e.g., in cases of inflammation and to
PT induce cancer cell differentiation.
XX
PS Claim 12; Fig 15A-F; 187pp; English.
XX
CC AAQ83235 depicts the nt. sequence compiled from sequencing cDNA clones
CC corresp. to the alpha-3 EpA transcript. The invention includes nt
CC sequences in the gp. comprising the nt sequence shown in AAQ83235, the
CC cDNA clone Ep-1 (ATCC No. 75540) shown in AAQ83234, the cDNA clone 1-1
CC (ATCC No. 75539), and the cDNA clone 8-6 (ATCC No. 75538), or the nt.
CC sequences shown in AAQ83236. The entire nt region encoding E170 is
CC depicted in AAQ83236, and corresp. to the SQ of alpha-3. AAQ83236
CC consists of a composite sequence derived from several overlapping clones.
CC A synthetic polypeptide of at least 5 AAs that corresp. to part or all of
CC the nt. sequence shown in AAQ83236 is claimed. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 1713 AA;

Query Match 79.1%; Score 3552.5; DB 2; Length 1713;
Best Local Similarity 78.3%; Pred. No. 1.5e-306;
Matches 679; Conservative 86; Mismatches 99; Indels 3; Gaps 2;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||||||: ||||||||:||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :||||||||||: ||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSPLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| |||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIHIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||:||||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130
```

```
Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1368

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| ||||||||||||::|:|||| :||||: |||:||:|||:: ||:||||
Db       1369 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1428

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |   |||
Db       1429 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 1488

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | |||||| :|||||::|||:|||| :||: |||| |||| |||||||: ||||
Db       1489 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1548

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || ||||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1549 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1608

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:||||||||||||||:||| ||||
Db       1609 SVTPKQSLCDGQWHSVAVTIKQHILHL 1635


RESULT 14
AAG75103
ID   AAG75103 standard; protein; 469 AA.
XX
AC   AAG75103;
XX
DT   03-SEP-2001  (first entry)
XX
DE   Human colon cancer antigen protein SEQ ID NO:5867.
XX
KW   Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW   colorectal carcinoma; chromosome 18.
XX
OS   Homo sapiens.
XX
PN   WO200122920-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-US026524.
XX
PR   29-SEP-1999;   99US-0157137P.
PR   03-NOV-1999;   99US-0163280P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Barash SC,  Birse CE,  Rosen CA;
XX
DR   WPI; 2001-235357/24.
DR   N-PSDB; AAH34508.
XX
PT   Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT   useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS   Claim 11; Page 7385-7387; 9803pp; English.
XX
CC   AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC   cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC   proteins are collectively known as colon cancer antigens. The colon
CC   cancer antigens have cytostatic activity and can be used in gene therapy
CC   and vaccine production. N and P may be used in the prevention, diagnosis
CC   and treatment of diseases associated with inappropriate P expression. For
CC   example, N and P may be used to treat disorders associated with decreased
CC   expression by rectifying mutations or deletions in a patient's genome
CC   that affect the activity of P by expressing inactive proteins or to
CC   supplement the patients own production of P. Additionally, N may be used
CC   to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC   into a host cell and culturing the cell to express the proteins. N and P
CC   can be used in the prevention, diagnosis and treatment of colorectal
CC   carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC   sequences used in the exemplification of the present invention. N.B.
CC   Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC   time of publication, meaning no sequences are present for SEQ ID NO:1027
CC   to 1052, 7921 and 7922
XX
SQ   Sequence 469 AA;

  Query Match             35.6%;  Score 1599;  DB 4;  Length 469;
  Best Local Similarity   65.9%;  Pred. No. 3.6e-133;
  Matches  323;  Conservative   55;  Mismatches   82;  Indels   30;  Gaps    5;

Qy        379 TASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELS 438
              :|||||  |:|||:| :|  ||   | |||||||||||| ||:||| |   | ||||||:||||
Db          1 SASFSRGXQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQTWTRXLQVTLEDGYIELS 60

Qy        439 TRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQQSLRLG 498
              | ||  |||||| ||||||||:|||||| ||||||||||:|| ::||   |:::||||||
Db         61 TSDSXGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLRNSKRLKHISSSRQSLRLG 120

Qy        499 GGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNKGR 558
              | :|||||||| ||| | ||||||| | | |:| ||||||||||||||| |   |||| :
Db        121 GSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLNKPPFLMLLKGSTRFNKTK 180

Qy        559 IFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQFGDSPTSHLLLKLPQELL 617
               | :|||:|| | |: || : |||  :| |   |:|:| |||||| |||||| |||||||
Db        181 TFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQFGDIPTSHLLFKLPQELL 238

Qy        618 KPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALGAGGKKLRLRSKERYHDG 677
              ||||||::|:|||| :||||: |||:||:|||:: ||:|||||  |||||::|||: :||
Db        239 KPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFALGTDGKKLRIKSKEKCNDG 298

Qy        678 KWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYLGLPLSRKPKSLPQHSFVG 737
              |||||||| :| | |||||||||:|||||||||| |  |||| | | |||||| :||||
Db        299 KWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYLGSPPSGKPKSLPTNSFVG 358

Qy        738 CLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHVILANSVSLGPELKLTFSI 797
              ||::|||:|||| :||: |||| |||| ||||||||: ||||:||:|| |||| || |||
Db        359 CLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHVVLAHSVLLGPEFKLVFSI 418

Qy        798 RPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTSITPKQSLCDGQW----- 852
              |||||||:|||:||| |  | : :  |:                |   |||
Db        419 RPRSLTGILIHIGSQPGXAL-MCLPGGR-----------------KGHGLYGQWGRWDL 459

Qy        853 ---HSVAVSI 859
                 |: |||:
Db        460 NVGHTKAVSV 469


RESULT 15
AAW26584
ID   AAW26584 standard; protein; 770 AA.
XX
AC   AAW26584;
XX
DT   25-MAR-2003  (revised)
DT   21-JAN-1998  (first entry)
XX
DE   Rat hemidesmosome formation inducing protein 154 kDa subunit.
XX
```

KW Hemidesmosome; laminin; epithelial cell; cell attachment; adhesion;
KW bladder carcinoma; 804G; NBT-II; rat; dental implant.
XX
OS Rattus sp.
XX
PN US5658789-A.
XX
PD 19-AUG-1997.
XX
PF 19-MAY-1995; 95US-00445135.
XX
PR 12-NOV-1993; 93US-00151134.
XX
PA (DESM-) DESMOS INC.
XX
PI Hormia M, Quaranta V;
XX
DR WPI; 1997-424242/39.
XX
PT Soluble protein that induces hemi:desmosome formation in epithelial cells
PT - useful for stimulating epithelial cell attachment, e.g. to dental
PT implants or teeth.
XX
PS Claim 2; Col 21-26; 20pp; English.
XX
CC This polypeptide comprises the 154 kDa alpha chain of an isolated soluble
CC protein that induces hemidesmosome formation in epithelial cells normally
CC unable to form hemidesmosomes. The 146 kD gamma chain (see AAW26584) and
CC the N-terminal portion (see AAW26585) of the 139 kDa beta chain sequence
CC were also determined. The protein has properties including: (a)
CC solubility in aqueous media; (b) binding by antibodies present in the
CC serum of rabbits inoculated with an extracellular matrix deposited by
CC 804G rat bladder carcinoma cells or NBT-II rat bladder carcinoma cells;
CC (c) being bound by monoclonal antibodies generated against extracellular
CC matrix; (d) promoting rapid epithelial cell adhesion to substrates coated
CC with at least one of the three protein chains; and (e) being obtainable
CC from 804G rat bladder carcinoma cells or NBT-II rat bladder carcinoma
CC cells. The protein (secreted laminin) is used to induce hemidesmosome
CC formation in epithelial cells and to facilitate their growth (claimed).
CC It may be used to promote cell attachment to solid surfaces, e.g. to
CC dental implants, and may also be of use in studies concerning
CC hemidesmosome morphogenesis and alpha 6 beta 4 integrin interactions with
CC the epithelial extracellular matrix. (Updated on 25-MAR-2003 to correct
CC PF field.)
XX
SQ Sequence 770 AA;

Query Match 29.2%; Score 1310; DB 2; Length 770;
Best Local Similarity 90.9%; Pred. No. 4.9e-107;
Matches 259; Conservative 3; Mismatches 13; Indels 10; Gaps 4;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 550

Qy         61 MA----VVDGQLTCVYNLGDREAEVQIDQV-LTESESQEAVMDRVKFQRIYQFAKLNYTK 115
              :      |    |:   | |   |   |: ||||||||||||||||||||||||||||
Db        551 IGGCRWPAD---VCLQPGGPR--SVSSDRSGLTESESQEAVMDRVKFQRIYQFAKLNYTK 605

Qy        116 EATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELD 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 EATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELD 665

Qy        176 DLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQT 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 DLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQT 725

Qy        236 IQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGI 280
              ||||| |||||||||||||||||||||||||||||||||||||||
Db        726 IQTTVARGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGI 770
```

Search completed: February 22, 2005, 08:18:44

Job time : 164.651 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:19:00 ; Search time 116.062 Seconds
(without alignments)
2441.722 Million cell updates/sec

Title: US-10-817-423-2
Perfect score: 4491
Sequence: 1 MRFNGKSGVEVRLPNDLEDL.....LCDGQWHSVAVSIKQRILHL 866

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4491	100.0	1694	15	US-10-603-725-12	Sequence 12, Appl
2	4491	100.0	1725	15	US-10-603-725-10	Sequence 10, Appl
3	3560.5	79.3	1693	15	US-10-603-725-4	Sequence 4, Appli
4	3560.5	79.3	1693	15	US-10-603-725-8	Sequence 8, Appli
5	3560.5	79.3	1713	14	US-10-171-311-113	Sequence 113, App
6	3560.5	79.3	1713	15	US-10-372-683-10	Sequence 10, Appl
7	3560.5	79.3	1713	15	US-10-603-725-6	Sequence 6, Appli
8	3560.5	79.3	1724	15	US-10-603-725-2	Sequence 2, Appli
9	1599	35.6	469	14	US-10-106-698-5877	Sequence 5877, Ap
10	1198	26.7	1816	15	US-10-372-683-4	Sequence 4, Appli
11	1192	26.5	1823	15	US-10-363-616-457	Sequence 457, App
12	1190	26.5	1581	16	US-10-408-765A-154	Sequence 154, App
13	1187	26.4	1816	14	US-10-299-058-2	Sequence 2, Appli
14	1185	26.4	1816	14	US-10-299-058-4	Sequence 4, Appli
15	1045.5	23.3	1634	15	US-10-037-417-49	Sequence 49, Appl
16	1045.5	23.3	1677	15	US-10-112-944-801	Sequence 801, App
17	1045.5	23.3	3695	15	US-10-312-352-22	Sequence 22, Appl
18	1045.5	23.3	3696	15	US-10-312-088-31	Sequence 31, Appl
19	1045.5	23.3	3705	15	US-10-312-088-30	Sequence 30, Appl
20	1042.5	23.2	3695	14	US-10-037-182-2	Sequence 2, Appli
21	1042	23.2	1640	15	US-10-037-417-8	Sequence 8, Appli
22	1041	23.2	3690	15	US-10-112-944-347	Sequence 347, App
23	1015.5	22.6	953	9	US-09-845-583-4	Sequence 4, Appli
24	1015.5	22.6	953	15	US-10-037-417-50	Sequence 50, Appl
25	948	21.1	3635	9	US-09-845-583-2	Sequence 2, Appli
26	948	21.1	3635	14	US-10-037-182-4	Sequence 4, Appli
27	948	21.1	3635	15	US-10-037-417-47	Sequence 47, Appl
28	943	21.0	3597	15	US-10-037-417-6	Sequence 6, Appli
29	943	21.0	3600	15	US-10-037-417-2	Sequence 2, Appli
30	908	20.2	908	15	US-10-037-417-4	Sequence 4, Appli
31	636.5	14.2	3712	13	US-10-108-605-103	Sequence 103, App
32	636.5	14.2	3712	15	US-10-037-417-48	Sequence 48, Appl
33	636.5	14.2	3712	15	US-10-037-417-51	Sequence 51, Appl
34	600.5	13.4	3672	15	US-10-369-493-6146	Sequence 6146, Ap
35	545	12.1	3084	9	US-09-938-275-4	Sequence 4, Appli
36	545	12.1	3084	14	US-10-262-670-2	Sequence 2, Appli
37	529.5	11.8	3075	9	US-09-938-275-5	Sequence 5, Appli
38	484.5	10.8	3070	10	US-09-961-403-7	Sequence 7, Appli
39	323.5	7.2	1514	15	US-10-336-603A-36	Sequence 36, Appl
40	322.5	7.2	296	14	US-10-299-058-5	Sequence 5, Appli
41	322.5	7.2	296	14	US-10-299-058-6	Sequence 6, Appli
42	321	7.1	289	14	US-10-299-058-13	Sequence 13, Appl
43	316	7.0	463	15	US-10-264-049-3039	Sequence 3039, Ap
44	314.5	7.0	342	15	US-10-264-049-3068	Sequence 3068, Ap
45	313.5	7.0	1399	15	US-10-187-975-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-10-603-725-12
; Sequence 12, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boutand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1694
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-603-725-12

Query Match 100.0%; Score 4491; DB 15; Length 1694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 810

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 870

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 930

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        931 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 990

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 1050

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 1110

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 1170

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 1230

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 1290

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQF 1350

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALG 1410

Qy        661 AGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYLG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1411 AGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYLG 1470

Qy        721 LPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1471 LPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHVI 1530

Qy        781 LANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTS 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1531 LANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTS 1590

Qy        841 ITPKQSLCDGQWHSVAVSIKQRILHL 866
              ||||||||||||||||||||||||||
Db       1591 ITPKQSLCDGQWHSVAVSIKQRILHL 1616
```

RESULT 2
US-10-603-725-10
; Sequence 10, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boutand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-603-725-10

Query Match 100.0%; Score 4491; DB 15; Length 1725;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 841
```

```
Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 901

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 961

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 1021

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 1081

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 1141

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 1201

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 1261

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 1321

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQF 1381

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALG 1441

Qy        661 AGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYLG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 AGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYLG 1501

Qy        721 LPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1502 LPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHVI 1561

Qy        781 LANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTS 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 LANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTS 1621

Qy        841 ITPKQSLCDGQWHSVAVSIKQRILHL 866
              ||||||||||||||||||||||||||
Db       1622 ITPKQSLCDGQWHSVAVSIKQRILHL 1647
```

RESULT 3
US-10-603-725-4
; Sequence 4, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boutand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1693
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-603-725-4

Query Match 79.3%; Score 3560.5; DB 15; Length 1693;
Best Local Similarity 78.4%; Pred. No. 5.1e-283;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||: |||||||:|||||||||||||:||||
Db        751 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 810

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        811 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 870

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||||
Db        871 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 930

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        931 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 990

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db        991 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1050

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||:|||||||||||||||||
Db       1051 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1110

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1111 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1170

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1171 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1230

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1231 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1290

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1291 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1348

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| |||||||||||::|:|||| :|||: |||:||:|||:: ||:||||
Db       1349 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1408

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       1409 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRARAGSLPGNSTISIRAPVYL 1468

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :||||||::|||:|||| :||: |||| |||| |||||||: ||||
Db       1469 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1528

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || ||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1529 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1588

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:||||||||||||||:||| ||||
Db       1589 SVTPKQSLCDGQWHSVAVTIKQHILHL 1615


RESULT 4
US-10-603-725-8
; Sequence 8, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
;  APPLICANT: Boutand, Ariel
;  TITLE OF INVENTION: Recombinant Laminin 5
;  FILE REFERENCE: 99-274-C
;  CURRENT APPLICATION NUMBER: US/10/603,725
;  CURRENT FILING DATE:  2003-06-25
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 1693
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-603-725-8

Query Match 79.3%; Score 3560.5; DB 15; Length 1693;
Best Local Similarity 78.4%; Pred. No. 5.1e-283;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||: |||||||:|||||||||||||:||||
Db        751 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 810

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        811 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 870

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||||
Db        871 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 930

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        931 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 990

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db        991 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1050

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||:|||||||||||||||||
Db       1051 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1110

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1111 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1170

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1171 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1230

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1231 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1290

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1291 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1348

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| |||||||||||::|:|||| :|||: |||:||:|||:: ||:||||
Db       1349 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1408

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       1409 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRARAGSLPGNSTISIRAPVYL 1468

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :||||||::|||:|||| :||: |||| |||| |||||||: ||||
Db       1469 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1528

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || ||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1529 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1588

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
```

```
                |:||||||||||||||||:||| ||||
Db       1589 SVTPKQSLCDGQWHSVAVTIKQHILHL 1615


RESULT 5
US-10-171-311-113
; Sequence 113, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
;  APPLICANT: Schlegel, Robert
;  APPLICANT:  Chen, Yan
;  APPLICANT:  Zhao, Xumei
;  APPLICANT:  Monahan, John
;  APPLICANT:  Kamatkar, Shubhangi
;  APPLICANT:  Glatt, Karen
;  APPLICANT:  Gannavarapu, Manjula
;  APPLICANT:  Hoersh, Sebastian
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
;  TITLE OF INVENTION:  OF CERVICAL CANCER
;  FILE REFERENCE: MRI-035
;  CURRENT APPLICATION NUMBER: US/10/171,311
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: US 60/298,159
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,155
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/335,936
;  PRIOR FILING DATE: 2001-11-14
;  NUMBER OF SEQ ID NOS: 238
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 113
;   LENGTH: 1713
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-171-311-113

  Query Match             79.3%;  Score 3560.5;  DB 14;  Length 1713;
  Best Local Similarity   78.4%;  Pred. No. 5.2e-283;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| |||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||||:|||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| |||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ::||   |:::|||||||| :|||||||| ||| | |||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1368

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| ||||||||||||::|:|||| :||||: |||:||:|||:: ||:||||
Db       1369 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1428

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       1429 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 1488

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :|||||::|||:|||| :||: |||| |||| |||||||: ||||
Db       1489 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1548

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || ||||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1549 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1608

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:||||||||||||||:||| ||||
Db       1609 SVTPKQSLCDGQWHSVAVTIKQHILHL 1635


RESULT 6
US-10-372-683-10
; Sequence 10, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
;  APPLICANT: GERRITSEN, MARY E.
;  APPLICANT:  PEALE JR., FRANKLIN V.
;  APPLICANT:  WU, THOMAS D.
;  TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
;  FILE REFERENCE: P1928R1P1
;  CURRENT APPLICATION NUMBER: US/10/372,683
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US 10/271,690
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/344,534
;  PRIOR FILING DATE: 2001-10-18
;  NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 10
;   LENGTH: 1713
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-372-683-10

  Query Match             79.3%;  Score 3560.5;  DB 15;  Length 1713;
  Best Local Similarity   78.4%;  Pred. No. 5.2e-283;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| |||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
```

```
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360

Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420

Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480

Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540

Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599

Db       1311 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1368

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659

Db       1369 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1428

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719

Db       1429 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRARREGSLPGNSTISIRAPVYL 1488

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779

Db       1489 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1548

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839

Db       1549 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1608

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866

Db       1609 SVTPKQSLCDGQWHSVAVTIKQHILHL 1635
```

RESULT 7
US-10-603-725-6
; Sequence 6, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boutand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1713
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-725-6

Query Match 79.3%; Score 3560.5; DB 15; Length 1713;
Best Local Similarity 78.4%; Pred. No. 5.2e-283;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60

Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120

Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180

Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240

Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300

Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360

Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420

Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480

Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540

Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599

Db       1311 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1368

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659

Db       1369 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1428

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719

Db       1429 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 1488

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779

Db       1489 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1548

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839

Db       1549 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1608

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866

Db       1609 SVTPKQSLCDGQWHSVAVTIKQHILHL 1635
```

RESULT 8
US-10-603-725-2
; Sequence 2, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boutand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1724
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-725-2

Query Match 79.3%; Score 3560.5; DB 15; Length 1724;

```
  Best Local Similarity   78.4%;  Pred. No. 5.3e-283;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        782 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 841

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        842 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 901

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db        902 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 961

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        962 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1021

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||| ||||:|: | ||:|:|||| | |||||
Db       1022 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1081

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||:|||||||||||||||||
Db       1082 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1141

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1142 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1201

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1202 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1261

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||||| :|||||||| ||| | ||||||| | | |:| |||||||||
Db       1262 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1321

Qy        541 KPPPLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| ||||
Db       1322 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1379

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| ||||||||||||::|:|||| :||||: |||:||:|||:: ||:||||
Db       1380 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1439

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       1440 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRARAGSLPGNSTISIRAPVYL 1499

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :||||||::|||:|||| :||: |||| |||| ||||||||: ||||
Db       1500 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1559

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || ||||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1560 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1619

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:|||||||||||||:||| ||||
Db       1620 SVTPKQSLCDGQWHSVAVTIKQHILHL 1646


RESULT 9
US-10-106-698-5877
; Sequence 5877, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
;  FILE REFERENCE: PA005P1
;  CURRENT APPLICATION NUMBER: US/10/106,698
;  CURRENT FILING DATE:  2002-03-27
;  PRIOR APPLICATION NUMBER: PCT/US00/26524
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US 60/157,137
;  PRIOR FILING DATE: 1999-09-29
;  PRIOR APPLICATION NUMBER: US 60/163,280
;  PRIOR FILING DATE: 1999-11-03
;  NUMBER OF SEQ ID NOS: 8564
;  SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 5877
;   LENGTH: 469
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (8)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (47)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (65)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (436)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5877

  Query Match           35.6%;  Score 1599;  DB 14;  Length 469;
  Best Local Similarity   65.9%;  Pred. No. 1.7e-122;
  Matches  323;  Conservative   55;  Mismatches   82;  Indels   30;  Gaps    5;

Qy        379 TASPFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELS 438
              :|||||| |:|||:| :| ||  | |||||||||||| ||:||| |  | |||||:||||
Db          1 SASPFSRGXQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQTWTRXLQVTLEDGYIELS 60

Qy        439 TRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQQSLRLG 498
              | ||  |||||| ||||||||:|||||| ||||||||||:|| ::||   |:::||||||
Db         61 TSDSXGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLRNSKRLKHISSSRQSLRLG 120

Qy        499 GGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNKGR 558
              | :|||||||| ||| | ||||||| | | |:| ||||||||||||||| |   |||| :
Db        121 GSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLNKPPFLMLLKGSTRFNKTK 180

Qy        559 IFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQFGDSPTSHLLLKLPQELL 617
              | :|||:|| | |: || : |||  :| |   |:|:| |||||| |||||| |||||||
Db        181 TFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQFGDIPTSHLLFKLPQELL 238

Qy        618 KPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALGAGGKKLRLRSKERYHDG 677
              ||||||::|:|||| :||||: |||:||:|||:: ||:|||||  |||||::|||: :||
Db        239 KPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFALGTDGKKLRIKSKEKCNDG 298

Qy        678 KWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYLGLPLSRKPKSLPQHSFVG 737
              |||||||| :| | |||||||||:|||||||||| |  |||| | | |||||| :||||
Db        299 KWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYLGSPPSGKPKSLPTNSFVG 358

Qy        738 CLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHVILANSVSLGPELKLTFSI 797
              ||::|||:|||| :||: |||| |||| ||||||||: ||||:||:|| |||| || |||
Db        359 CLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHVVLAHSVLLGPEFKLVFSI 418

Qy        798 RPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTSITPKQSLCDGQW----- 852
              |||||||:|||:||| |  | : :  |:                    |     |||
Db        419 RPRSLTGILIHIGSQPGXAL-MCLPGGR-----------------KGHGLYGQWGRWDL 459

Qy        853 ---HSVAVSI 859
                 |: |||:
Db        460 NVGHTKAVSV 469


RESULT 10
US-10-372-683-4
; Sequence 4, Application US/10372683
; Publication No. US20040009171A1
```

; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: PEALE JR., FRANKLIN V.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 4
; LENGTH: 1816
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-372-683-4

Query Match 26.7%; Score 1198; DB 15; Length 1816;
Best Local Similarity 33.1%; Pred. No. 1.5e-88;
Matches 309; Conservative 161; Mismatches 373; Indels 90; Gaps 26;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFL----QRPDLRENGGTEDMFVMYLGNKDASK 56
              | |:|:| |||      ::||| :|||||::    :||:| |   | | |::|||:|:| |
Db        829 MMFDGQSAVEVHSRTSMDDLKAFTSLSLYMKPPVKRPELTE---TADQFILYLGSKNAKK 885

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
              :|:|:|: :  |  ||||| :: |: :|       |  |     || :|: :  |: |
Db        886 EYMGLAIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVP 943

Qy        117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDD 176
              : |:  :   :   |    ::||:|||| |||||| | :|:||: |  | : ||:||
Db        944 SLSSTAEEKFIKKGEFSGDDSLLDLDPEDTVFYVGGVPSNFKLPTSLNLPGFVGCLELAT 1003

Qy        177 LNENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYARIPTQPN----A 227
              || :|:|||||  :|:: :   || | |       :   :|:|:|||  :   |
Db       1004 LNNDVISLYNFKHIYNMDPSTSVPCARDKLAFTQSRAASYFFDGSGYAVVRDIPRRGKFG 1063

Qy        228 PFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRY-------KLNSEPPKEKGI 280
                |  ::|  | ||:    |  | | : :| | | |       ::: |  :|
Db       1064 QVTRFDIEVRTPADNGLILLMVNGSMFFRLEMRNGYLHVFYDFGFSSGRVHLEDTLKKA- 1122

Qy        281 RDTINDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIP------I 331
              |||| | | | |     |:| : |: | |:      |     |:  |:|| |
Db       1123 --QINDAKYHEISI-IYHNDKKMILVVDRRHVKSMDNEKMKIPFTDIYIGGAPPEILQSR 1179

Qy        332 AIRERFNISTPAFQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQM 388
              |:|    :    |:|||      ||   ::   :|:||   | ||  : | | |:  ||
Db       1180 ALRAHLPLDI-NFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQS 1236

Qy        389 SFTNLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIF 447
              ::  :   | |:  | |:| ||:| |  : : :    ::|::| : :  :   | :
Db       1237 FIASIQKISFFDGFEGGFNFRTLQPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQ 1294

Qy        448 KSPGTYMDGLLHHVSVISDTSGLR--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-- 499
                | ||| |   |||  |  |  |::|  :|  :|       | | :
Db       1295 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSP 1352

Qy        500 -----GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
                  :| |||||    |  :  || |    : |   ||  | :   |  :| |  |
Db       1353 ISAQYANFTGCISNAYFTRVDRDVEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNL 1412

Qy        555 NKGRIFNVNQ--LMQDAPQATRSTEAWQDGRSCLPPLNT------------KASHRALQF 600
              :| :    :   :|||          :|        || ||           :|   | |:
Db       1413 SKPKASQNKKGGKSKDAP-------SWDPVALKLPERNTPRNSHCHLSNSPRAIEHAYQY 1465

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKD--SFLALYVADGRVVFA 658
              | :  |    :  :     :||||: ::|  |  |::||   ::    |: |::| ||:|:
Db       1466 GGTANSRQEFEHLKGDFGAKSQFSIRLRTRSSHGMIFYVSDQEENDFMTLFLAHGRLVYM 1525

Qy        659 LGAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSL-PGNSTISPREQV 717
                | |||::||:|:|:|| || |:|        |||:||||  | || |  :|   :  :
```

```
Db       1526 FNVGHKKLKIRSQEKYNDGLWHDVIFIRERSSGRLVIDGLRVLEESLPPTEATWKIKGPI 1585

Qy        718 YLGLPLSRKPKSLPQ----HSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFS 773
              |||      |      |    :|| ||| : |||   : | |  | |:||  | :| | |||
Db       1586 YLGGVAPGKAVKNVQINSIYSFSGCLSNLQLNGASITSASQTFSVTPCFEGPMETGTYFS 1645

Qy        774 QGGGHVILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSD 833
              ||:|:|  | ::| : :: | :|||| :| |:|  | :|: |:|:|: |:|   |::
Db       1646 TEGGYVVLDESFNIGLKFEIAFEVRPRSSSGTLVHGHSVNGEYLNVHMKNGQVIVKVNNG 1705

Qy        834 AGGSVTSITPKQSLCDGQWHSVAVSIKQRILHL 866
                ||:||||||||:|| : |      :: |
Db       1706 IRDFSTSVTPKQSLCDGRWHRITVIRDSNVVQL 1738
```

RESULT 11
US-10-363-616-457
; Sequence 457, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 457
; LENGTH: 1823
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-457

Query Match 26.5%; Score 1192; DB 15; Length 1823;
Best Local Similarity 33.5%; Pred. No. 4.7e-88;
Matches 312; Conservative 158; Mismatches 374; Indels 88; Gaps 28;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFL----QRPDLRENGGTEDMFVMYLGNKDASK 56
              | |:|:| |||      ::||| :|||||::    :||:| |   | | |::|||:|:| |
Db        836 MMFDGQSAVEVHSRTSMDDLKAFTSLSLYMKPPVKRPELTE---TADQFILYLGSKNAKK 892

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
              :|:|:|: :  |  ||||| :: |: :|       |  |     || :|: :  |: |
Db        893 EYMGLAIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVP 950

Qy        117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDD 176
              : |:  :   :   |    ::||:|||| |||||| | :|:||: |  | : ||:||
Db        951 SLSSTAEEKFIKKGEFSGDDSLLDLDPEDTVFYVGGVPSNFKLPTSLNLPGFVGCLELAT 1010

Qy        177 LNENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYA--RIPTQPN--A 227
              || :|:|||||  :|:: :   || | |       :   :|:|:|||  |  |:
Db       1011 LNNDVISLYNFKHIYNMDPSTSVPCARDKLAFTQSRAASYFFDGSGYAVVRDITRRGKFG 1070

Qy        228 PFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLN-SEPPKEKGIRDT--- 283
                |  ::|  | ||:    |  | | : :| | | |       |  |  : ||
Db       1071 QVTRFDIEVRTPADNGLILLMVNGSMFFRLEMRNGYLHVFYDFGFSSGPVH--LEDTLKK 1128

Qy        284 --INDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIP------IA 332
                ||| | | | | |     |:| : |: | |:      |     |:  |:|| |      |
Db       1129 AQINDAKYHEISI-IYHNDKKMILVVDRRHVKSMDNEKMKIPFTDIYIGGAPPEILQSRA 1187

Qy        333 IRERFNISTPAFQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMS 389
              :|    :    |:|||      ||   ::   :|:||   | ||  : | | |:  ||
Db       1188 LRAHLPLDI-NFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSF 1244

Qy        390 FTNLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFK 448
              ::  :   | |:  | |:| ||:| |  : : :    ::|::| : :  :   | :
Db       1245 IASIQKISFFDGFEGGFNFRTLQPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQS 1302

Qy        449 SPGTYMDGLLHHVSVISDTSGLR--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG--- 499
                | ||| |   |||  |  |  |::|  :|  :|       | | :
Db       1303 VDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSPI 1360
```

```
Qy        500 ----GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFN 555
Db       1361 SAQYANFTGCISNAYFTRVDRDVEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNLS 1420

Qy        556 KGRIFNVNQ--LMQDAPQATRSTEAWQDGRSCLPPLNT------------KASHRALQFG 601
Db       1421 KPKASQNKKGGKSKDAP-------SWDPVALKLPERNTPRNSHCHLSNSPRAIEHAYQYG 1473

Qy        602 DSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKD--SFLALYVADGRVVFAL 659
Db       1474 GTANSRQEFEHLKGDFGAKSQFSIRLRTRSSHGMIFYVSDQEENDFMTLFLAHGRLVYMF 1533

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSL-PGNSTISPREQVY 718
Db       1534 NVGHKKLKIRSQEKYNDGLWHDVIFIRERSSGRLVIDGLRVLEESLPPTEATWKIKGPIY 1593

Qy        719 LGLPLSRKPKSLPQ----HSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQ 774
Db       1594 LGGVAPGKAVKNVQINSIYSFSGCLSNLQLNGASITSASQTFSVTPCFEGPMETGTYFST 1653

Qy        775 GGGHVILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDA 834
Db       1654 EGGYVVLDESFNIGLKFEIAFEVRPRSSSGTLVHGHSVNGEYLNVHMKNGQVIVKVNNGI 1713

Qy        835 GGSVTSITPKQSLCDGQWHSVAVSIKQRILHL 866
Db       1714 RDFSTSVTPKQSLCDGRWHRITVIRDSNVVQL 1745


RESULT 12
US-10-408-765A-154
; Sequence 154, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
;  APPLICANT: Ghosh, Soumitra S.
;  APPLICANT:  Fahy, Eoin D.
;  APPLICANT:  Zhang, Bing
;  APPLICANT:  Gibson, Bradford W.
;  APPLICANT:  Taylor, Steven W.
;  APPLICANT:  Glenn, Gary M.
;  APPLICANT:  Warnock, Dale E.
;  TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
;  TITLE OF INVENTION:  IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
;  FILE REFERENCE: 660088.465
;  CURRENT APPLICATION NUMBER: US/10/408,765A
;  CURRENT FILING DATE:  2003-04-04
;  NUMBER OF SEQ ID NOS: 3077
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 154
;   LENGTH: 1581
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-765A-154

  Query Match             26.5%;  Score 1190;  DB 16;  Length 1581;
  Best Local Similarity   33.2%;  Pred. No. 5.4e-88;
  Matches  310;  Conservative  161;  Mismatches  372;  Indels   90;  Gaps   27;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFL----QRPDLRENGGTEDMFVMYLGNKDASK 56
Db        594 MMFDGQSAVEVHSRTSMDDLKAFTSLSLYMKPPVKRPELTE---TADQFILYLGSKNAKK 650

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
Db        651 EYMGLAIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVP 708

Qy        117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDD 176
Db        709 SLSSTAEEKFIKKGEFSGDDSLLDLDPEDTVFYVGGVPSNFKLPTSLNLPGFVGCLELAT 768

Qy        177 LNENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYA--RIPTQPN--A 227
Db        769 LNNDVISLYNFKHIYNMDPSTSVPCARDKLAFTQSRAASYFFDGSGYAVVRDITRRGKFG 828

Qy        228 PFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRY-------KLNSEPPKEKGI 280
Db        829 QVTRFDIEVRTPADNGLILLLMVNGSMFFRLEMRNGYLHVFYDFGFSSGRVHLEDTLKKA- 887

Qy        281 RDTINDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIP------I 331
Db        888 --QINDAKYHEISI-IYHNDKKMILVVDRRHVKSMDNEKMKIPFTDIYIGGAPPEILQSR 944

Qy        332 AIRERFNISTPAFQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQM 388
Db        945 ALRAHLPLDI-NFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQS 1001

Qy        389 SFTNLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIF 447
Db       1002 FIASIQKISFFDGFEGGFNFRTLQPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQ 1059

Qy        448 KSPGTYMDGLLHHVSVISDTSGLR--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-- 499
Db       1060 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSP 1117

Qy        500 -----GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
Db       1118 ISAQYANFTGCISNAYFTRVDRDVEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNL 1177

Qy        555 NKGRIFNVNQ--LMQDAPQATRSTEAWQDGRSCLPPLNT------------KASHRALQF 600
Db       1178 SKPKASQNKKGGKSKDAP-------SWDPVALKLPERNTPRNSHCHLSNSPRAIEHAYQY 1230

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKD--SFLALYVADGRVVFA 658
Db       1231 GGTANSRQEFEHLKGDFGAKSQFSIRLRTRSSHGMIFYVSDQEENDFMTLFLAHGRLVYM 1290

Qy        659 LGAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSL-PGNSTISPREQV 717
Db       1291 FNVGHKKLKIRSQEKYNDGLWHDVIFIRERSSGRLVIDGLRVLEESLPPTEATWKIKGPI 1350

Qy        718 YLGLPLSRKPKSLPQ----HSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFS 773
Db       1351 YLGGVAPGKAVKNVQINSIYSFSGCLSNLQLNGASITSASQTFSVTPCFEGPMETGTYFS 1410

Qy        774 QGGGHVILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSD 833
Db       1411 TEGGYVVLDESFNIGLKFEIAFEVRPRSSSGTLVHGHSVNGEYLNVHMKNGQVIVKVNNG 1470

Qy        834 AGGSVTSITPKQSLCDGQWHSVAVSIKQRILHL 866
Db       1471 IRDFSTSVTPKQSLCDGRWHRITVIRDSNVVQL 1503


RESULT 13
US-10-299-058-2
; Sequence 2, Application US/10299058
; Publication No. US20030103975A1
; GENERAL INFORMATION:
;  APPLICANT: JONES, JONATHAN C.R.
;  APPLICANT:  GONZALES, MEREDITH
;  TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHELIALIZATION
;  FILE REFERENCE: 1720-1-002 CIP
;  CURRENT APPLICATION NUMBER: US/10/299,058
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 09/706,235
;  PRIOR FILING DATE: 2000-11-03
;  PRIOR APPLICATION NUMBER: 60/163,199
;  PRIOR FILING DATE: 1999-11-03
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1816
;   TYPE: PRT
;   ORGANISM: Homo sapien
;   FEATURE:
```

```
;  OTHER INFORMATION: X in position 1112 = Arg/Pro
US-10-299-058-2

  Query Match             26.4%;  Score 1187;  DB 14;  Length 1816;
  Best Local Similarity   33.2%;  Pred. No. 1.2e-87;
  Matches  310;  Conservative  160;  Mismatches  373;  Indels   90;  Gaps   27;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFL----QRPDLRENGGTEDMFVMYLGNKDASK 56
              | |:|:| |||     ::||| :|||||::    :||:| |   | | |::|||:|:| |
Db        829 MMFDGQSAVEVHSRTSMDDLKAFTSLSLYMKPPVKRPELTE---TADQFILYLGSKNAKK 885

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
             :|:|:|: :  |  ||||| :: |: :|       |  |     || :|: :  |:  |
Db        886 EYMGLAIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVP 943

Qy        117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDD 176
             : |:  :   :   |    ::||:|||| |||||| | :|:||: |  | : ||:||
Db        944 SLSSTAEEKPIKKGEFSGDDSLLDLDPEDTVFYVGGVPSNFKLPTSLNLPGFVGCLELAT 1003

Qy        177 LNENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYA--RIPTQPN--A 227
             || :|:|||||  :|:: :   || | |       :   :|:|:|||  |  |:
Db       1004 LNNDVISLYNFKHIYNMDPSTSVPCARDKLAFTQSRAASYFFDGSGYAVVRDITRRGKFG 1063

Qy        228 PFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRY-------KLNSEPPKEKGI 280
                 ::|  | ||:    |   | | : :| | | |         :: |   :|
Db       1064 QVTRFDIEVRTPADNGLILLMVNGSMFFRLEMRNGYLHVFYDFGFSSGXVHLEDTLKKA- 1122

Qy        281 RDTINDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIP------I 331
               ||| | | | |     :|: : |: | |:     |      |:  |:|| |
Db       1123 --QINDAKYHEISI-IYHNDKKMILVVDRRHVKSMDNEKMKIPFTDIYIGGAPPEILQSR 1179

Qy        332 AIRERFNISTPAFQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQM 388
             |:|    :    |:||||     ||   ::   :|:||   | ||  : | |:  ||
Db       1180 ALRAHLPLDI-NFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQS 1236

Qy        389 SFTNLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIF 447
               ::  :   | |:  | |:| ||:| |  : : :    ::|::| : :  :   | :
Db       1237 FIASIQKISFFDGFEGGFNFRTLQPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQ 1294

Qy        448 KSPGTYMDGLLHHVSVISDTSGLR--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-- 499
               | ||| |   |||  |  |  |::|  :|  :|      | |  :    ||
Db       1295 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSP 1352

Qy        500 -----GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
                  :| |||||    |  :  || |    : |   ||  | :   |  :| |   |
Db       1353 ISAQYANFTGCISNAYFTRVDRDVEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNL 1412

Qy        555 NKGRIFNVNQ--LMQDAPQATRSTEAWQDGRSCLPPLNT------------KASHRALQF 600
             :| :     :    :|||       :|       ||  ||             :|   | |:
Db       1413 SKPKASQNKKGGKSKDAP-------SWDPVALKLPERNTPRNSHCHLSNSPRAIEHAYQY 1465

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKD--SFLALYVADGRVVFA 658
             | :  |    :  :    :||||: ::| |  |::||   ::   |: |::| ||:|:
Db       1466 GGTANSRQEPEHLKGDFGAKSQFSIRLRTRSSHGMIFYVSDQEENDFMTLFLAHGRLVYM 1525

Qy        659 LGAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSL-PGNSTISPREQV 717
             | |||::||:|:|:|| || |:|       |||:|||| | || |  :|   :  :
Db       1526 FNVGHKKLKIRSQEKYNDGLWHDVIFIRERSSGRLVIDGLRVLEESLPPTEATWKIKGPI 1585

Qy        718 YLGLPLSRKPKSLPQ----HSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFS 773
             |||      |      :|| ||| : |||   : | |  | |:||  | :| | |||
Db       1586 YLGGVAPGKAVKNVQINSIYSFSGCLSNLQLNGASITSASQTFSVTPCFEGPMETGTYFS 1645

Qy        774 QGGGHVILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSD 833
               ||:|:|  | ::| : :: | :|||| :| |:|  | :|: |:|:|: |:|   |::
Db       1646 TEGGYVVLDESFNIGLKFEIAFEVRPRSSSGTLVHGHSVNGEYLNVHMKNGQVIVKVNNG 1705

Qy        834 AGGSVTSITPKQSLCDGQWHSVAVSIKQRILHL 866
               ||:|||||||||:|| : |      :: |
Db       1706 IRDFSTSVTPKQSLCDGRWHRITVIRDSNVVQL 1738


RESULT 14
US-10-299-058-4
; Sequence 4, Application US/10299058
; Publication No. US20030103975A1
; GENERAL INFORMATION:
;  APPLICANT: JONES, JONATHAN C.R.
;  APPLICANT:  GONZALES, MEREDITH
;  TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHELIALIZATION
;  FILE REFERENCE: 1720-1-002 CIP
;  CURRENT APPLICATION NUMBER: US/10/299,058
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 09/706,235
;  PRIOR FILING DATE: 2000-11-03
;  PRIOR APPLICATION NUMBER: 60/163,199
;  PRIOR FILING DATE: 1999-11-03
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1816
;   TYPE: PRT
;   ORGANISM: Homo sapien
;   FEATURE:
;   OTHER INFORMATION: X in position 1112 = R/P
US-10-299-058-4

  Query Match             26.4%;  Score 1185;  DB 14;  Length 1816;
  Best Local Similarity   33.2%;  Pred. No. 1.7e-87;
  Matches  310;  Conservative  160;  Mismatches  373;  Indels   90;  Gaps   27;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFL----QRPDLRENGGTEDMFVMYLGNKDASK 56
              | |:|:| |||     ::||| :|||||::    :||:| |   | | |::|||:|:| |
Db        829 MMFDGQSAVEVHSRTSMDDLKAFTSLSLYMKPPVKRPELTE---TADQFILYLGSKNAKK 885

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
             :|:|:|: :  |  ||||| :: |: :|       |  |     || :|: :  |:  |
Db        886 EYMGLAIKNDNLVYVYNLGTKDVEIPLDS--KPVGSWPAYFSIVKIERVGKHGKVFLTVP 943

Qy        117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDD 176
             : |:  :   :   |    ::||:|||| |||||| | :|:||: |  | : ||:||
Db        944 SLSSTAEEKFIKKGEFSGDDSLLDLDPEDTVFYVGGVPSNFKLPTSLNLPGFVGCLELAT 1003

Qy        177 LNENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYA--RIPTQPN--A 227
             || :|:|||||  :|:: :   || | |       :   :|:|:|||  |  |:
Db       1004 LNNDVISLYNFKHIYNMDPSTSVPCARDKLAFTQSRAASYFFDGSGYAVVRDITRRGKFG 1063

Qy        228 PFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRY-------KLNSEPPKEKGI 280
                 ::|  | ||:    |   | | : :| | | |         :: |   :|
Db       1064 QVTRFDIEVRTPADNGLILLMVNGSMFFRLEMRNGYLHVFYDFGFSSGXVHLEDTLKKA- 1122

Qy        281 RDTINDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIP------I 331
               ||| | | | |     :|: : |: | |:     |      |:  |:|| |
Db       1123 --QINDAKYHEISI-IYHNDKKMILVVDRRHVKSMDNEKMKIPFTDIYIGGAPPEILQSR 1179

Qy        332 AIRERFNISTPAFQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQM 388
             |:|    :    |:||||     ||   ::   :|:||   | ||  : | |:  ||
Db       1180 ALRAHLPLDI-NFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQS 1236

Qy        389 SFTNLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIF 447
               ::  :   | |:  | |:| ||:| |  : : :    ::|::| : :  :   | :
Db       1237 FIASIQKISFFDGFEGGFNFRTLQPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQ 1294

Qy        448 KSPGTYMDGLLHHVSVISDTSGLR--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-- 499
               | ||| |   |||  |  |  |::|  :|  :|      | |  :    ||
Db       1295 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSP 1352

Qy        500 -----GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
                  :| |||||    |  :  || |    : |   ||  | :   |  :| |   |
Db       1353 ISAQYANFTGCISNAYFTRVDRDVEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNL 1412

Qy        555 NKGRIFNVNQ--LMQDAPQATRSTEAWQDGRSCLPPLNT------------KASHRALQF 600
             :| :     :    :|||       :|       ||  ||             :|   | |:
Db       1413 SKPKASQNKKGGKSKDAP-------SWDPVALKLPERNTPRNSHCHLSNSPRAIEHAYQY 1465

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKD--SFLALYVADGRVVFA 658
```

```
Db       1466 GGTANSRQEFEHLKGDFGAKSQFSIRLRTRSSHGMIFYVSDQEENDFMTLFLAHGRLVYM 1525

Qy        659 LGAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSL-PGNSTISPREQV 717

Db       1526 FNVGHKKLKIRSQEKYNDGLWHDVIFIRERSSGRLVIDGLRVLEESLPPTEATWKIKGPI 1585

Qy        718 YLGLPLSRKPKSLPQ----HSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFS 773

Db       1586 YLGGVAPGKAVKNVQINSIYSFSGCLSNLQLNGASITSASQTFSVTPCFEGPMETGTYFS 1645

Qy        774 QGGGHVILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSD 833

Db       1646 TEGGYVVLDESFNIGLKFEIAFEVRPRSSSGTLVHGHSVNGEYLNVHMKNGQVIVKVNNG 1705

Qy        834 AGGSVTSITPKQSLCDGQWHSVAVSIKQRILHL 866

Db       1706 IRDFSTSVTPKQSLCDGRWHRITVIRDSNVVQL 1738


RESULT 15
US-10-037-417-49
; Sequence 49, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
;  APPLICANT: Kekuda, Ramesh
;  APPLICANT:  Alsobrook II, John P
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Lepley, Denise M
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Li, Li
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Edinger, Shlomit R
;  APPLICANT:  Sciore, Paul
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Rothenberg, Mark
;  APPLICANT:  Stone, David J
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Anderson, David W
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Miller, Charles E
;  APPLICANT:  Eisen, Andrew J
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-235
;  CURRENT APPLICATION NUMBER: US/10/037,417
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: 60/260,018
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: 60/260,360
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/272,411
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/272,817
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: 60/291,186
;  PRIOR FILING DATE: 2001-05-15
;  PRIOR APPLICATION NUMBER: 60/303,231
;  PRIOR FILING DATE: 2001-07-05
;  PRIOR APPLICATION NUMBER: 60/305,060
;  PRIOR FILING DATE: 2001-07-12
;  PRIOR APPLICATION NUMBER: 60/318,405
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: 60/318,700
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
;   LENGTH: 1634
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-037-417-49

  Query Match             23.3%;  Score 1045.5;  DB 15;  Length 1634;
  Best Local Similarity   31.6%;  Pred. No. 4.4e-76;
  Matches  294;  Conservative  159;  Mismatches  367;  Indels  109;  Gaps   32;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60

Db        676 MKFNGRSGVQLRTPRDLADLAAYTALKFYLQGPEPEPGQGTEDRFVMYMGSRQATGDYMG 735

Qy         61 MAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE--- 116

Db        736 VSLRDKKVHWVYQLGEAGPAVLSIDEDIGEQ------FAAVSLDRTLQFGHMSVTVERQM 789

Qy        117 --ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIEL 174

Db        790 IQETKGDTVAPGA---EG-----LLNLRPDDFVFYVGGYPSTFTPPPLLRFPGYRGCIEM 841

Qy        175 DDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPN-AP 228

Db        842 DTLNEEVVSLYNFERTFQLDTAVDRPCARSKSTGDPWLTDGSYLDGTGFARISFDSQIST 901

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPP----- 275

Db        902 TKRFEQELRLVSYSGVLFFLKQQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPPLTS 961

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNER---SVRIEGEIFDFSTYYLGGI--- 329

Db        962 ASKAIQ-----------VFLLGGSRKRVLVRVERATVYSVEQDNDLELADAYYLGGVPPD 1010

Qy        330 --PIAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSR 384

Db       1011 QLPPSLRRLFP-TGGSVRGCVKGIKALGKYVDLKRLN-TTGVSAGCTADLLVGRAMTFHG 1068

Qy        385 GG--QMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDS 442

Db       1069 HGFLRLALSNV-APLTGNVYSGFGFHSAQDSALLYYRASPDGLCQVSLQQGRVSLQLLRT 1127

Qy        443 NIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQV--LRRNQRLPSFSNAQQS----LR 496

Db       1128 EV---KTQAGFADGAPHYVAFYSNATGVWLYVDDQLQQMKPHRGPPPELQPQPEGPPRLL 1184

Qy        497 LGG-------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFK 549

Db       1185 LGGLPESGTIYNFSGCISNVFVQRLLGPQRVFDLQQNLGSVNVST-GCA----PALQA-Q 1238

Qy        550 SPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQFGDSPTSHLL 609

Db       1239 TPGLGPRG-------LQATARKASRRSRQPARHPACMLPPHLRTTRDSYQFGGSLSSH-- 1289

Qy        610 LKLPQELLKPRS--QFSLDIQTTSPKGLVFYAG---TKDSFLALYVADGRVVFALGAGGK 664

Db       1290 LEFVGILARHRNWPSLSMHVLPRSSRGLLLFTARLRPGSPSLALFLSNGHFVAQMEGLGT 1349

Qy        665 KLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRA--QEG---SLPGNSTISPREQVYL 719

Db       1350 RLRAQSRQRSRPGRWHKVSVRWEKNRILLVTDGARAWSQEGPHRQHQGAEHPQPHTLFVG 1409

Qy        720 GLPLSRKPKSLP-QHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGH 778

Db       1410 GLPASSHSSKLPVTVGFSGCVKRLRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGV 1469

Qy        779 VILANSVSLGPELKLTFSIRPRSLTGVLIHVG-SQSGQRLSVYMEAGKVTTSVSSDAGGS 837

Db       1470 ITLDLPGATLPDVGLELEVRPLAVTGLIFHLGQARTPPYLQLQVTEKQVLLRADDGAGEF 1529

Qy        838 VTSITPKQSLCDGQWHSVAVSIKQRILHL 866
```

```
              ||:|    ||||||| :||     :| |
Db       1530 STSVTRPSVLCDGQWHRLAVMKSGNVLRL 1558
```

Search completed: February 22, 2005, 08:44:39
Job time : 119.062 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:13:40 ; Search time 40.4378 Seconds
(without alignments)
1598.653 Million cell updates/sec

Title: US-10-817-423-2
Perfect score: 4491
Sequence: 1 MRFNGKSGVEVRLPNDLEDL.....LCDGQWHSVAVSIKQRILHL 866

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4491	100.0	1694	4	US-09-560-385A-12	Sequence 12, Appl
2	4491	100.0	1725	4	US-09-560-385A-10	Sequence 10, Appl
3	3560.5	79.3	1693	4	US-09-560-385A-4	Sequence 4, Appli
4	3560.5	79.3	1693	4	US-09-560-385A-8	Sequence 8, Appli
5	3560.5	79.3	1713	3	US-08-600-982-24	Sequence 24, Appl
6	3560.5	79.3	1713	4	US-09-560-385A-6	Sequence 6, Appli
7	3560.5	79.3	1713	4	US-09-538-092-1359	Sequence 1359, Ap
8	3560.5	79.3	1713	5	PCT-US94-10261A-24	Sequence 24, Appl
9	3560.5	79.3	1724	4	US-09-560-385A-2	Sequence 2, Appli
10	1310	29.2	770	1	US-08-445-135-2	Sequence 2, Appli
11	1198	26.7	1792	4	US-09-561-818A-4	Sequence 4, Appli
12	1198	26.7	1800	4	US-09-561-818A-8	Sequence 8, Appli
13	1198	26.7	1816	4	US-09-561-818A-2	Sequence 2, Appli
14	1198	26.7	1824	4	US-09-561-818A-6	Sequence 6, Appli
15	1183	26.3	1792	4	US-09-561-818A-12	Sequence 12, Appl
16	1183	26.3	1816	4	US-09-561-818A-10	Sequence 10, Appl
17	1015.5	22.6	953	4	US-09-845-583A-4	Sequence 4, Appli
18	948	21.1	3635	4	US-09-845-583A-2	Sequence 2, Appli
19	925	20.6	3647	4	US-09-949-016-10932	Sequence 10932, A
20	534.5	11.9	1130	6	5444158-2	Patent No. 5444158
21	534.5	11.9	1130	6	5444158-2	Patent No. 5444158
22	530.5	11.8	3075	2	US-08-460-309-5	Sequence 5, Appli
23	530.5	11.8	3075	2	US-08-125-077-5	Sequence 5, Appli
24	526.5	11.7	1130	2	US-08-460-309-2	Sequence 2, Appli
25	526.5	11.7	1130	2	US-08-125-077-2	Sequence 2, Appli
26	526.5	11.7	3088	4	US-09-562-702A-8	Sequence 8, Appli
27	526.5	11.7	3089	4	US-09-562-702A-4	Sequence 4, Appli
28	526.5	11.7	3110	4	US-09-562-702A-2	Sequence 2, Appli
29	526.5	11.7	3110	4	US-09-562-702A-6	Sequence 6, Appli
30	526.5	11.7	3110	4	US-09-561-709B-7	Sequence 7, Appli
31	526.5	11.7	3110	4	US-09-917-254-86	Sequence 86, Appl
32	526.5	11.7	3110	4	US-09-949-016-5937	Sequence 5937, Ap
33	526.5	11.7	3111	2	US-08-460-309-4	Sequence 4, Appli
34	526.5	11.7	3111	2	US-08-125-077-4	Sequence 4, Appli
35	516.5	11.5	3084	4	US-09-562-702A-12	Sequence 12, Appl
36	516.5	11.5	3106	4	US-09-562-702A-10	Sequence 10, Appl
37	484.5	10.8	3070	4	US-09-961-403-7	Sequence 7, Appli
38	294	6.5	1384	4	US-09-949-016-7814	Sequence 7814, Ap
39	220.5	4.9	1331	4	US-09-949-016-6861	Sequence 6861, Ap
40	205	4.6	1384	4	US-08-826-134-2	Sequence 2, Appli
41	205	4.6	1384	4	US-09-949-016-6395	Sequence 6395, Ap
42	183	4.1	4391	4	US-10-006-011A-2	Sequence 2, Appli
43	180	4.0	705	4	US-10-006-011A-3	Sequence 3, Appli
44	176.5	3.9	1058	4	US-09-949-016-11457	Sequence 11457, A
45	174	3.9	1381	4	US-08-826-134-4	Sequence 4, Appli

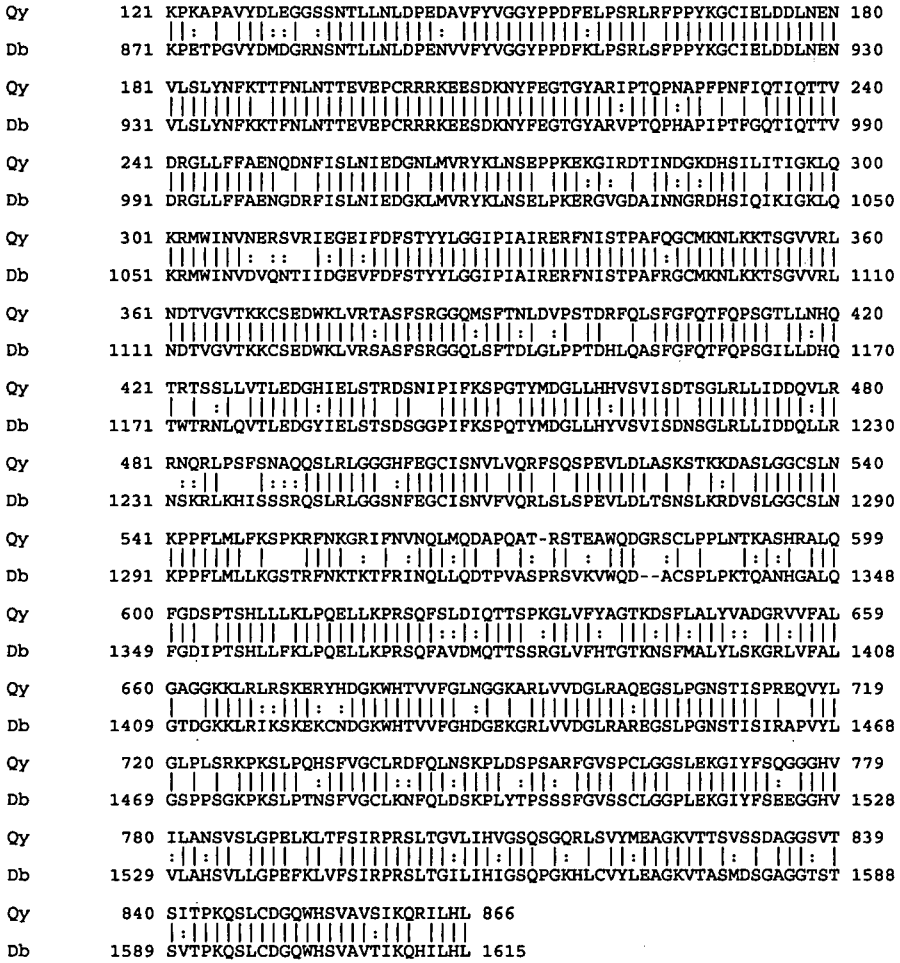
ALIGNMENTS

RESULT 1
US-09-560-385A-12
; Sequence 12, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Boutand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1694
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-560-385A-12

Query Match 100.0%; Score 4491; DB 4; Length 1694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

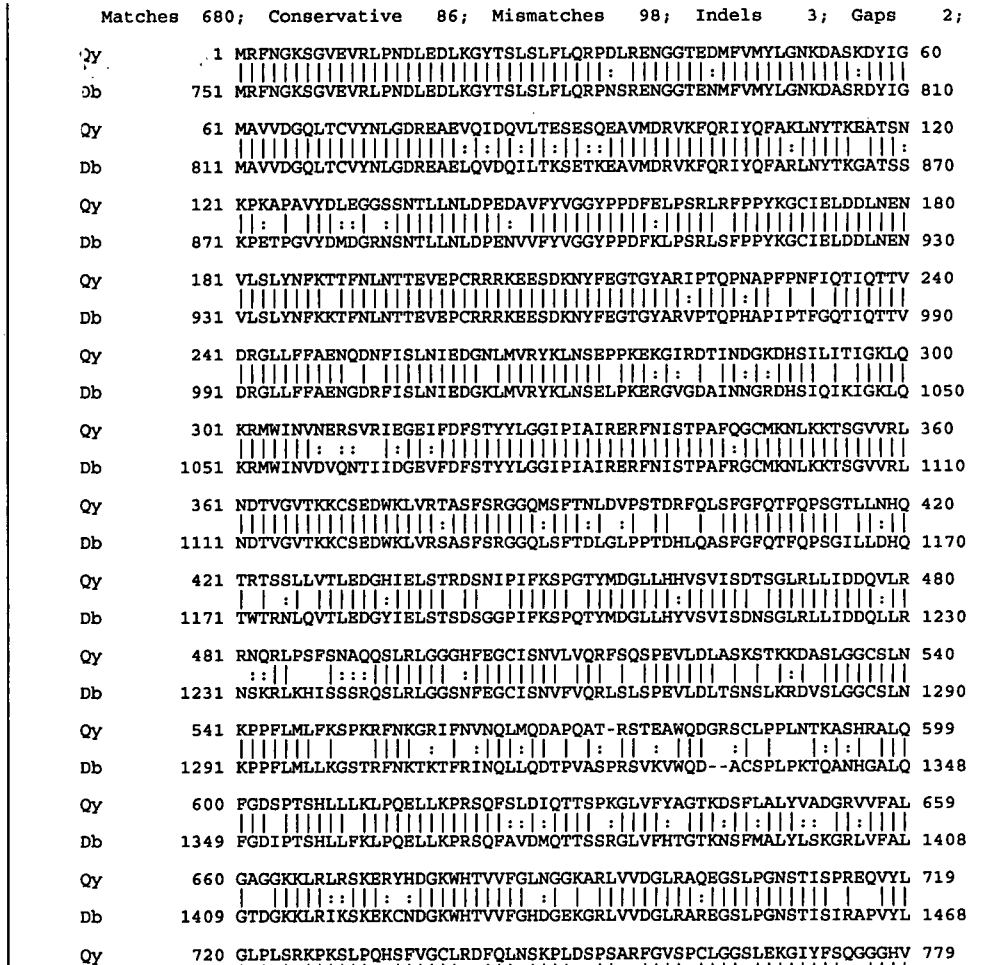
```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 810

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 870

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 930

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 990

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 1050

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 1110

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 1170
```

```
Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 1230

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 1290

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQF 1350

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALG 1410

Qy        661 AGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYLG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1411 AGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYLG 1470

Qy        721 LPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1471 LPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHVI 1530

Qy        781 LANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTS 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1531 LANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTS 1590

Qy        841 ITPKQSLCDGQWHSVAVSIKQRILHL 866
              ||||||||||||||||||||||||||
Db       1591 ITPKQSLCDGQWHSVAVSIKQRILHL 1616


RESULT 2
US-09-560-385A-10
; Sequence 10, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
;  APPLICANT:  Boutand, Ariel
;  TITLE OF INVENTION:  Recombinant Laminin 5
;  FILE REFERENCE:  99-274-C
;  CURRENT APPLICATION NUMBER: US/09/560,385A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 1725
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-560-385A-10

  Query Match             100.0%;  Score 4491;  DB 4;  Length 1725;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  866;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 841

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 901

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 961

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 1021

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 1081

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 1141

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 1201

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 1261

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 1321

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQATRSTEAWQDGRSCLPPLNTKASHRALQF 1381

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFALG 1441

Qy        661 AGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYLG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 AGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYLG 1501

Qy        721 LPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1502 LPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHVI 1561

Qy        781 LANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTS 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 LANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVTS 1621

Qy        841 ITPKQSLCDGQWHSVAVSIKQRILHL 866
              ||||||||||||||||||||||||||
Db       1622 ITPKQSLCDGQWHSVAVSIKQRILHL 1647


RESULT 3
US-09-560-385A-4
; Sequence 4, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
;  APPLICANT:  Boutand, Ariel
;  TITLE OF INVENTION:  Recombinant Laminin 5
;  FILE REFERENCE:  99-274-C
;  CURRENT APPLICATION NUMBER: US/09/560,385A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1693
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-560-385A-4

  Query Match             79.3%;  Score 3560.5;  DB 4;  Length 1693;
  Best Local Similarity   78.4%;  Pred. No. 0;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        751 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 810

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              |||||||||||||||||||:|:||:||:||::||||||||||||||:||||| |||:
Db        811 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 870
```



RESULT 4
US-09-560-385A-8
; Sequence 8, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Boutand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1693
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-385A-8

Query Match 79.3%; Score 3560.5; DB 4; Length 1693;
Best Local Similarity 78.4%; Pred. No. 0;



RESULT 5
US-08-600-982-24
; Sequence 24, Application US/08600982
; Patent No. 6120991
; GENERAL INFORMATION:
; APPLICANT: Carter, William G.
; APPLICANT: Gil, Susanna A.
; APPLICANT: Ryan, Maureen C.
; TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for
; TITLE OF INVENTION: Integrins

```
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen, O'Connor, Johnson, and Kindness
;      STREET:  1420 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101-8100
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/600,982
;      FILING DATE:  02-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Shelton, Dennis K.
;      REGISTRATION NUMBER:  26,997
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 682-8100
;      TELEFAX:  (206) 224-0779
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1713 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;      DESCRIPTION:  E170 protein as translated from sequence
;      DESCRIPTION:  of FIGURES 15A-15F, and as shown also in FIGURES
;      DESCRIPTION:  19A-19R
US-08-600-982-24

  Query Match            79.3%;  Score 3560.5;  DB 3;  Length 1713;
  Best Local Similarity  78.4%;  Pred. No. 0;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||||||: |||||||:|||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              |||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| |||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||:|||||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||:|||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::||||||| :|||||||| ||| | |||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1368

Qy        600 PGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| |||||||||||||::|:|||| :||||: |||:||:|||:: ||:||||
Db       1369 PGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1428

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  ||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       1429 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 1488

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :|||||::|||:|||| :||: |||| |||| ||||||||: ||||
Db       1489 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1548

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || ||||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1549 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1608

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:||||||||||||||||:||| ||||
Db       1609 SVTPKQSLCDGQWHSVAVTIKQHILHL 1635


RESULT 6
US-09-560-385A-6
; Sequence 6, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
;  APPLICANT:  Boutand, Ariel
;  TITLE OF INVENTION:  Recombinant Laminin 5
;  FILE REFERENCE:  99-274-C
;  CURRENT APPLICATION NUMBER: US/09/560,385A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 1713
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-560-385A-6

  Query Match            79.3%;  Score 3560.5;  DB 4;  Length 1713;
  Best Local Similarity  78.4%;  Pred. No. 0;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||||||: |||||||:|||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              |||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| |||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||:|||||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
```

```
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480

Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540

Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599

Db       1311 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1368

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659

Db       1369 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1428

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719

Db       1429 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 1488

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779

Db       1489 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1548

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839

Db       1549 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1608

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866

Db       1609 SVTPKQSLCDGQWHSVAVTIKQHILHL 1635
```

RESULT 7
US-09-538-092-1359
; Sequence 1359, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1359
; LENGTH: 1713
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q16787
US-09-538-092-1359

Query Match 79.3%; Score 3560.5; DB 4; Length 1713;
Best Local Similarity 78.4%; Pred. No. 0;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60

Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120

Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180

Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240

Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300

Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360

Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420

Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480

Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540

Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599

Db       1311 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1368

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659

Db       1369 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1428

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719

Db       1429 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 1488

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779

Db       1489 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1548

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839

Db       1549 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1608

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866

Db       1609 SVTPKQSLCDGQWHSVAVTIKQHILHL 1635
```

RESULT 8
PCT-US94-10261A-24
; Sequence 24, Application PC/TUS9410261A
; GENERAL INFORMATION:
; APPLICANT: Carter, William G.
; APPLICANT: Gil, Susanna A.
; APPLICANT: Ryan, Maureen C.
; TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for
; TITLE OF INVENTION: Integrins
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness
; STREET: 1420 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-8100
; COMPUTER READABLE FORM:

```
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/10261A
;       FILING DATE:  02-SEP-1994
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Shelton, Dennis K.
;       REGISTRATION NUMBER:  26,997
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 682-8100
;       TELEFAX:  (206) 224-0779
;   INFORMATION FOR SEQ ID NO:  24:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1713 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;       DESCRIPTION:  E170 protein as translated from sequence of
;       DESCRIPTION:  FIGURES 15A-15F, and as shown also in FIGURES 19A-19R
PCT-US94-10261A-24

  Query Match             79.3%;  Score 3560.5;  DB 5;  Length 1713;
  Best Local Similarity   78.4%;  Pred. No. 0;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||: |||||||:|||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| |||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||||||:||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ::||   |:::|||||||| :|||||||| ||| | ||||||| | | |:| |||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1368

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| ||||||||||||::|:|||| :||||: |||:||:|||:: ||:||||
Db       1369 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1428

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||||| |  |||
Db       1429 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 1488

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :|||||||::|||:|||| :||: |||| |||| |||||||||: ||||
Db       1489 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1548

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || ||||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1549 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1608

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:||||||||||||||:||| ||||
Db       1609 SVTPKQSLCDGQWHSVAVTIKQHILHL 1635


RESULT 9
US-09-560-385A-2
; Sequence 2, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
;  APPLICANT:  Boutand, Ariel
;  TITLE OF INVENTION:  Recombinant Laminin 5
;  FILE REFERENCE:  99-274-C
;  CURRENT APPLICATION NUMBER: US/09/560,385A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1724
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-560-385A-2

  Query Match             79.3%;  Score 3560.5;  DB 4;  Length 1724;
  Best Local Similarity   78.4%;  Pred. No. 0;
  Matches  680;  Conservative   86;  Mismatches   98;  Indels    3;  Gaps    2;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||: |||||||:|||||||||||||:||||
Db        782 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 841

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::||||||||||||||:||||| |||:
Db        842 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 901

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| |||||||||||||||||
Db        902 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 961

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        962 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1021

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||| |||:|: | ||:|:|||| | |||||
Db       1022 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1081

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||||||:||||||||||||||
Db       1082 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1141

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1142 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1201

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1202 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1261

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ::||   |:::|||||||| :|||||||| ||| | ||||||| | | |:| |||||||||
Db       1262 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1321
```

```
Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQLMQDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
              ||||||| |   |||| : | :|||:|| | |: || : |||  :| |   |:|:| |||
Db       1322 KPPFLMLLKGSTRFNKTKTFRINQLLQDTPVASPRSVKVWQD--ACSPLPKTQANHGALQ 1379

Qy        600 FGDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKDSFLALYVADGRVVFAL 659
              ||| |||||| ||||||||||||||::|:|||| :||||: |||:||:|||:: ||:||||
Db       1380 FGDIPTSHLLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVFAL 1439

Qy        660 GAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSLPGNSTISPREQVYL 719
              |  |||||::|||: :|||||||||| :| | |||||||||:|||||||||| |  |||
Db       1440 GTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPGNSTISIRAPVYL 1499

Qy        720 GLPLSRKPKSLPQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGGHV 779
              | | | |||||| :|||||::|||:|||| :||: |||| |||| |||||||: ||||
Db       1500 GSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFGVSSCLGGPLEKGIYFSEEGGHV 1559

Qy        780 ILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGSVT 839
              :||:|| |||| || ||||||||||:|||:||| |: | ||:|||||| |: | |||: |
Db       1560 VLAHSVLLGPEFKLVFSIRPRSLTGILIHIGSQPGKHLCVYLEAGKVTASMDSGAGGTST 1619

Qy        840 SITPKQSLCDGQWHSVAVSIKQRILHL 866
              |:||||||||||||||:||| ||||
Db       1620 SVTPKQSLCDGQWHSVAVTIKQHILHL 1646


RESULT 10
US-08-445-135-2
; Sequence 2, Application US/08445135
; Patent No. 5658789
;  GENERAL INFORMATION:
;    APPLICANT:  Quaranta, Vito
;    APPLICANT:  Hormia, Marketta
;    TITLE OF INVENTION:  Promotion of Epithelial Cell Adhesion
;    TITLE OF INVENTION:  and Hemidesmosome Assembly by a Laminin-Like Molecule
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson and Bear
;      STREET:  620 Newport Center Drive, Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/445,135
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/151,134
;      FILING DATE:  12-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Israelsen, Ned A.
;      REGISTRATION NUMBER:  29,655
;      REFERENCE/DOCKET NUMBER:  DESMOS.002CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 235-8550
;      TELEFAX:  (619) 235-0176
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  770 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    IMMEDIATE SOURCE:
;      CLONE:  150 kD
US-08-445-135-2

 Query Match           29.2%;  Score 1310;  DB 1;  Length 770;
 Best Local Similarity  90.9%;  Pred. No. 1.5e-121;
 Matches  259;  Conservative    3;  Mismatches   13;  Indels   10;  Gaps    4;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 550

Qy         61 MA----VVDGQLTCVYNLGDREAEVQIDQV-LTESESQEAVMDRVKFQRIYQFAKLNYTK 115
              :      |    |:   | |   |  |: ||||||||||||||||||||||||||||
Db        551 IGGCRWPAD---VCLQPGGPR--SVSSDRSGLTESESQEAVMDRVKFQRIYQFAKLNYTK 605

Qy        116 EATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELD 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 EATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELD 665

Qy        176 DLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQT 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 DLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQT 725

Qy        236 IQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGI 280
              ||||| ||||||||||||||||||||||||||||||||||||||
Db        726 IQTTVARGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGI 770


RESULT 11
US-09-561-818A-4
; Sequence 4, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
;  APPLICANT: Kortesmaa, Jarrko
;  APPLICANT:  Tryggvason, Karl
;  TITLE OF INVENTION: Laminin 8 and Methods For Its Use
;  FILE REFERENCE: 99,274-D
;  CURRENT APPLICATION NUMBER: US/09/561,818A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1792
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-561-818A-4

  Query Match           26.7%;  Score 1198;  DB 4;  Length 1792;
  Best Local Similarity  33.1%;  Pred. No. 1.1e-109;
  Matches  309;  Conservative  161;  Mismatches  373;  Indels   90;  Gaps   26;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFL----QRPDLRENGGTEDMFVMYLGNKDASK 56
              | |:|:| |||     ::||| :|||||::    :||:| |    | | |::|||:|:| |
Db        805 MMFDGQSAVEVHSRTSMDDLKAFTSLSLYMKPPVKRPELTE---TADQFILYLGSKNAKK 861

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
              :|:|:|: :  |  ||||| :: |: :|       |  |     || :|: :  |:  |
Db        862 EYMGLAIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVP 919

Qy        117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDD 176
              : |:  :   :    |    ::||:||||| |||||| | :|:||: |  | : ||:||
Db        920 SLSSTAEEKFIKKGEFSGDDSLLDLDPEDTVFYVGGVPSNFKLPTSLNLPGFVGCLELAT 979

Qy        177 LNENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYARIPTQPN----A 227
              || :|:|||||  :|:: :   || | |        :   :|:|:||| :   |
Db        980 LNNDVISLYNFKHIYNMDPSTSVPCARDKLAFTQSRAASYFFDGSGYAVVRDIPRRGKFG 1039

Qy        228 PFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRY-------KLNSEPPKEKGI 280
                |   ::|  | ||:    |   |  | : :| | | |         ::: |   :|
Db       1040 QVTRFDIEVRTPADNGLILLMVNGSMFFRLEMRNGYLHVFYDFGFSSGRVHLEDTLKKA- 1098

Qy        281 RDTINDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIP------I 331
                ||| | | | | |    |:| : |: | |:    |     |:  |:|| |
```

```
Db       1099 --QINDAKYHEISI-IYHNDKKMILVVDRRHVKSMDNEKMKIPFTDIYIGGAPPEILQSR 1155

Qy        332 AIRERFNISTPAFQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQM 388
              |:|     :    |:||||      ||    ::    :|:||    | ||  : | | |:  ||
Db       1156 ALRAHLPLDI-NFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQS 1212

Qy        389 SFTNLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIF 447
                ::  :   | |:  | |:| ||:|  |  : : :    ::|::| : :  :    | :
Db       1213 FIASIQKISFFDGFEGGFNFRTLQPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQ 1270

Qy        448 KSPGTYMDGLLHHVSVISDTSGLR--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-- 499
                | ||| |   |||  |  |  |::|  :|  :|          | | :    ||
Db       1271 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSP 1328

Qy        500 -----GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
                  :| |||||     |  :  || |    :  |   ||  | :    |  :| | |
Db       1329 ISAQYANFTGCISNAYFTRVDRDVEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNL 1388

Qy        555 NKGRIFNVNQ--LMQDAPQATRSTEAWQDGRSCLPPLNT------------KASHRALQF 600
                :| :    :    :|||       :|      ||  ||             :|   | |:
Db       1389 SKPKASQNKKGGKSKDAP-------SWDPVALKLPERNTPRNSHCHLSNSPRAIEHAYQY 1441

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKD--SFLALYVADGRVVFA 658
              | :  |    :  :     :||||: ::| |  |::||   ::    |: |::| ||:|:
Db       1442 GGTANSRQEFEHLKGDFGAKSQFSIRLRTRSSHGMIFYVSDQEENDFMTLFLAHGRLVYM 1501

Qy        659 LGAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSL-PGNSTISPREQV 717
                | |||::||:|:|:|| || |:|       |||:|||  | || |  :|  :  :
Db       1502 FNVGHKKLKIRSQEKYNDGLWHDVIFIRERSSGRLVIDGLRVLEESLPPTEATWKIKGPI 1561

Qy        718 YLGLPLSRKPKSLPQ----HSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFS 773
              |||     |    :|| ||| : |||   : | | :|:||  | :| | |||
Db       1562 YLGGVAPGKAVKNVQINSIYSFSGCLSNLQLNGASITSASQTFSVTPCFEGPMETGTYFS 1621

Qy        774 QGGGHVILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSD 833
                ||:|:|  | ::| : :: | :|||| :| |:|  | :|: |:|:|: |:|   |::
Db       1622 TEGGYVVLDESFNIGLKFEIAFEVRPRSSSGTLVHGHSVNGEYLNVHMKNGQVIVKVNNG 1681

Qy        834 AGGSVTSITPKQSLCDGQWHSVAVSIKQRILHL 866
                ||:||||||||:|| : |     :: |
Db       1682 IRDFSTSVTPKQSLCDGRWHRITVIRDSNVVQL 1714


RESULT 12
US-09-561-818A-8
; Sequence 8, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
;  APPLICANT: Kortesmaa, Jarrko
;  APPLICANT:  Tryggvason, Karl
;  TITLE OF INVENTION: Laminin 8 and Methods For Its Use
;  FILE REFERENCE: 99,274-D
;  CURRENT APPLICATION NUMBER: US/09/561,818A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 1800
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-561-818A-8

  Query Match             26.7%;  Score 1198;  DB 4;  Length 1800;
  Best Local Similarity   33.1%;  Pred. No. 1.1e-109;
  Matches  309;  Conservative  161;  Mismatches  373;  Indels   90;  Gaps   26;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFL----QRPDLRENGGTEDMFVMYLGNKDASK 56
              | |:|:|  |||     ::||| :|||||::    :||:| |   | | |::|||:|:| |
Db        805 MMFDGQSAVEVHSRTSMDDLKAFTSLSLYMKPPVKRPELTE---TADQFILYLGSKNAKK 861

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
              :|:|:|: :  |  ||||| :: |: :|       |  |     || :|: :  |:  |
Db        862 EYMGLAIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVP 919


Qy        117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDD 176
              : |:  :   :   |     ::||:|||||  |||||| | :|:||: |  | : ||:||
Db        920 SLSSTAEEKFIKKGEFSGDDSLLDLDPEDTVFYVGGVPSNFKLPTSLNLPGFVGCLELAT 979

Qy        177 LNENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYARIPTQPN----A 227
              || :|:|||||  :|:: :   || | |       :  :|:|:||| :    |
Db        980 LNNDVISLYNFKHIYNMDPSTSVPCARDKLAFTQSRAASYFFDGSGYAVVRDIPRRGKFG 1039

Qy        228 PFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRY-------KLNSEPPKEKGI 280
                |   ::|  | ||:   |   |  | : :| | | |        ::: |   :|
Db       1040 QVTRFDIEVRTPADNGLILLMVNGSMFFRLEMRNGYLHVFYDFGFSSGRVHLEDTLKKA- 1098

Qy        281 RDTINDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIP------I 331
              ||| | | | | |     |:| : |: | |:     |       |:  |:|| |
Db       1099 --QINDAKYHEISI-IYHNDKKMILVVDRRHVKSMDNEKMKIPFTDIYIGGAPPEILQSR 1155

Qy        332 AIRERFNISTPAFQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQM 388
              |:|     :    |:||||      ||    ::    :|:||    | ||  : | | |:  ||
Db       1156 ALRAHLPLDI-NFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQS 1212

Qy        389 SFTNLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIF 447
                ::  :   | |:  | |:| ||:|  |  : : :    ::|::| : :  :    | :
Db       1213 FIASIQKISFFDGFEGGFNFRTLQPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQ 1270

Qy        448 KSPGTYMDGLLHHVSVISDTSGLR--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-- 499
                | ||| |   |||  |  |  |::|  :|  :|          | | :    ||
Db       1271 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSP 1328

Qy        500 -----GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
                  :| |||||     |  :  || |    :  |   ||  | :    |  :| | |
Db       1329 ISAQYANFTGCISNAYFTRVDRDVEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNL 1388

Qy        555 NKGRIFNVNQ--LMQDAPQATRSTEAWQDGRSCLPPLNT------------KASHRALQF 600
                :| :    :    :|||       :|      ||  ||             :|   | |:
Db       1389 SKPKASQNKKGGKSKDAP-------SWDPVALKLPERNTPRNSHCHLSNSPRAIEHAYQY 1441

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKD--SFLALYVADGRVVFA 658
              | :  |    :  :     :||||: ::| |  |::||   ::    |: |::| ||:|:
Db       1442 GGTANSRQEFEHLKGDFGAKSQFSIRLRTRSSHGMIFYVSDQEENDFMTLFLAHGRLVYM 1501

Qy        659 LGAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSL-PGNSTISPREQV 717
                | |||::||:|:|:|| || |:|       |||:|||| | || |  :|  :  :
Db       1502 FNVGHKKLKIRSQEKYNDGLWHDVIFIRERSSGRLVIDGLRVLEESLPPTEATWKIKGPI 1561

Qy        718 YLGLPLSRKPKSLPQ----HSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFS 773
              |||     |    :|| ||| : |||   : | | :|:||  | :| | |||
Db       1562 YLGGVAPGKAVKNVQINSIYSFSGCLSNLQLNGASITSASQTFSVTPCFEGPMETGTYFS 1621

Qy        774 QGGGHVILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSD 833
                ||:|:|  | ::| : :: | :|||| :| |:|  | :|: |:|:|: |:|   |::
Db       1622 TEGGYVVLDESFNIGLKFEIAFEVRPRSSSGTLVHGHSVNGEYLNVHMKNGQVIVKVNNG 1681

Qy        834 AGGSVTSITPKQSLCDGQWHSVAVSIKQRILHL 866
                ||:||||||||:|| : |     :: |
Db       1682 IRDFSTSVTPKQSLCDGRWHRITVIRDSNVVQL 1714


RESULT 13
US-09-561-818A-2
; Sequence 2, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
;  APPLICANT: Kortesmaa, Jarrko
;  APPLICANT:  Tryggvason, Karl
;  TITLE OF INVENTION: Laminin 8 and Methods For Its Use
;  FILE REFERENCE: 99,274-D
;  CURRENT APPLICATION NUMBER: US/09/561,818A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1816
```

```
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-561-818A-2

  Query Match             26.7%;  Score 1198;  DB 4;  Length 1816;
  Best Local Similarity   33.1%;  Pred. No. 1.2e-109;
  Matches  309;  Conservative  161;  Mismatches  373;  Indels   90;  Gaps   26;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFL----QRPDLRENGGTEDMFVMYLGNKDASK 56
              | |:|:| |||     ::||| :||||||::    :||:| |   | | |::|||:|:| |
Db        829 MMFDGQSAVEVHSRTSMDDLKAFTSLSLYMKPPVKRPELTE---TADQFILYLGSKNAKK 885

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
             :|:|:|: :   |  ||||| :: |: :|        | |     || :|: :  |:  |
Db        886 EYMGLAIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVP 943

Qy        117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDD 176
             : |:  :   :    |    ::||:||||| |||||| | :|:||: |  | : ||:||
Db        944 SLSSTAEEKFIKKGEFSGDDSLLDLDPEDTVFYVGGVPSNFKLPTSLNLPGFVGCLELAT 1003

Qy        177 LNENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYARIPTQPN----A 227
             || :|:|||||| :|:: :   || | |       :  :|:|:||| :   |
Db       1004 LNNDVISLYNFKHIYNMDPSTSVPCARDKLAFTQSRAASYFFDGSGYAVVRDIPRRGKFG 1063

Qy        228 PFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRY-------KLNSEPPKEKGI 280
                |  ::|  | ||:     |   | | : :| | |         ::: |   :|
Db       1064 QVTRFDIEVRTPADNGLILLMVNGSMFFRLEMRNGYLHVFYDFGFSSGRVHLEDTLKKA- 1122

Qy        281 RDTINDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIP------I 331
               ||| | | | | |    |:| : |: | |:      |      |:  |:|| |
Db       1123 --QINDAKYHEISI-IYHNDKKMILVVDRRHVKSMDNEKMKIPFTDIYIGGAPPEILQSR 1179

Qy        332 AIRERFNISTPAFQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQM 388
             |:|    :    |:||||     ||   ::   :|:||   | ||  : | | |:  ||
Db       1180 ALRAHLPLDI-NFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQS 1236

Qy        389 SFTNLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIF 447
               ::  :   | |:  | |:| ||:| |  : : :    ::|::| : :  :   | :
Db       1237 FIASIQKISFFDGFEGGFNFRTLQPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQ 1294

Qy        448 KSPGTYMDGLLHHVSVISDTSGLR--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-- 499
               | ||| |   |||  |  |::|  :|  :|        | |  :     ||
Db       1295 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSP 1352

Qy        500 -----GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
                  :| |||||     |  :  || |     :  |    ||  | :   |  :| |  |
Db       1353 ISAQYANFTGCISNAYFTRVDRDVEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNL 1412

Qy        555 NKGRIFNVNQ--LMQDAPQATRSTEAWQDGRSCLPPLNT------------KASHRALQF 600
               :| :    :    :|||          :|      ||  ||              :|   | |:
Db       1413 SKPKASQNKKGGKSKDAP-------SWDPVALKLPERNTPRNSHCHLSNSPRAIEHAYQY 1465

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKD--SFLALYVADGRVVFA 658
               | :  |    :  :     :||||: ::| |  |::||   ::   |: |::| ||:|:
Db       1466 GGTANSRQEFEHLKGDFGAKSQFSIRLRTRSSHGMIFYVSDQEENDFMTLFLAHGRLVYM 1525

Qy        659 LGAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSL-PGNSTISPREQV 717
               | |||::||:|:|:|| || |:|        |||:|||| | || |  :|   :  :
Db       1526 FNVGHKKLKIRSQEKYNDGLWHDVIFIRERSSGRLVIDGLRVLEESLPPTEATWKIKGPI 1585

Qy        718 YLGLPLSRKPKSLPQ----HSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFS 773
               |||    |    |    :|| ||| : |||   : | |  | |:||  | :| | |||
Db       1586 YLGGVAPGKAVKNVQINSIYSFSGCLSNLQLNGASITSASQTFSVTPCFEGPMETGTYFS 1645

Qy        774 QGGGHVILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSD 833
               ||:|:|  | ::| : :: | :|||| :|  :|  | :|: |:|:|: |:|   |::
Db       1646 TEGGYVVLDESFNIGLKFEIAFEVRPRSSSGTLVHGHSVNGEYLNVHMKNGQVIVKVNNG 1705

Qy        834 AGGSVTSITPKQSLCDGQWHSVAVSIKQRILHL 866
                ||:||||||||:|| : |     :: |
Db       1706 IRDFSTSVTPKQSLCDGRWHRITVIRDSNVVQL 1738
```

```
RESULT 14
US-09-561-818A-6
; Sequence 6, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
;  APPLICANT: Kortesmaa, Jarrko
;  APPLICANT:  Tryggvason, Karl
;  TITLE OF INVENTION: Laminin 8 and Methods For Its Use
;  FILE REFERENCE: 99,274-D
;  CURRENT APPLICATION NUMBER: US/09/561,818A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 1824
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-561-818A-6

  Query Match             26.7%;  Score 1198;  DB 4;  Length 1824;
  Best Local Similarity   33.1%;  Pred. No. 1.2e-109;
  Matches  309;  Conservative  161;  Mismatches  373;  Indels   90;  Gaps   26;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFL----QRPDLRENGGTEDMFVMYLGNKDASK 56
              | |:|:| |||     ::||| :|||||::    :||:| |   | | |::|||:|:| |
Db        829 MMFDGQSAVEVHSRTSMDDLKAFTSLSLYMKPPVKRPELTE---TADQFILYLGSKNAKK 885

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
             :|:|:|: :   |  ||||| :: |: :|        | |     || :|: :  |:  |
Db        886 EYMGLAIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVP 943

Qy        117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDD 176
             : |:  :   :    |    ::||:||||| |||||| | :|:||: |  | : ||:||
Db        944 SLSSTAEEKFIKKGEFSGDDSLLDLDPEDTVFYVGGVPSNFKLPTSLNLPGFVGCLELAT 1003

Qy        177 LNENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYARIPTQPN----A 227
             || :|:|||||| :|:: :   || | |       :  :|:|:||| :   |
Db       1004 LNNDVISLYNFKHIYNMDPSTSVPCARDKLAFTQSRAASYFFDGSGYAVVRDIPRRGKFG 1063

Qy        228 PFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRY-------KLNSEPPKEKGI 280
                |  ::|  | ||:     |   | | : :| | |         ::: |   :|
Db       1064 QVTRFDIEVRTPADNGLILLMVNGSMFFRLEMRNGYLHVFYDFGFSSGRVHLEDTLKKA- 1122

Qy        281 RDTINDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIP------I 331
               ||| | | | | |    |:| : |: | |:      |      |:  |:|| |
Db       1123 --QINDAKYHEISI-IYHNDKKMILVVDRRHVKSMDNEKMKIPFTDIYIGGAPPEILQSR 1179

Qy        332 AIRERFNISTPAFQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQM 388
             |:|    :    |:||||     ||   ::   :|:||   | ||  : | | |:  ||
Db       1180 ALRAHLPLDI-NFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQS 1236

Qy        389 SFTNLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIF 447
               ::  :   | |:  | |:| ||:| |  : : :    ::|::| : :  :   | :
Db       1237 FIASIQKISFFDGFEGGFNFRTLQPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQ 1294

Qy        448 KSPGTYMDGLLHHVSVISDTSGLR--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-- 499
               | ||| |   |||  |  |::|  :|  :|        | |  :     ||
Db       1295 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSP 1352

Qy        500 -----GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
                  :| |||||     |  :  || |     :  |    ||  | :   |  :| |  |
Db       1353 ISAQYANFTGCISNAYFTRVDRDVEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNL 1412

Qy        555 NKGRIFNVNQ--LMQDAPQATRSTEAWQDGRSCLPPLNT------------KASHRALQF 600
               :| :    :    :|||          :|      ||  ||              :|   | |:
Db       1413 SKPKASQNKKGGKSKDAP-------SWDPVALKLPERNTPRNSHCHLSNSPRAIEHAYQY 1465

Qy        601 GDSPTSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKD--SFLALYVADGRVVFA 658
               | :  |    :  :     :||||: ::| |  |::||   ::   |: |::| ||:|:
Db       1466 GGTANSRQEFEHLKGDFGAKSQFSIRLRTRSSHGMIFYVSDQEENDFMTLFLAHGRLVYM 1525

Qy        659 LGAGGKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSL-PGNSTISPREQV 717
               | |||::||:|:|:|| || |:|        |||:|||| | || |  :|   :  :
```

```
Db       1526 FNVGHKKLKIRSQEKYNDGLWHDVIFIRERSSGRLVIDGLRVLEESLPPTEATWKIKGPI 1585

Qy        718 YLGLPLSRKPKSLPQ----HSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFS 773
              |||      |     |    :|| ||| : |||   : | | | |:||  | :| | |||
Db       1586 YLGGVAPGKAVKNVQINSIYSFSGCLSNLQLNGASITSASQTFSVTPCFEGPMETGTYFS 1645

Qy        774 QGGGHVILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSD 833
              ||:|:|  | ::| : :: | :|||| :| |:|  | :|: |:|:|: |:|   |::
Db       1646 TEGGYVVLDESFNIGLKFEIAFEVRPRSSSGTLVHGHSVNGEYLNVHMKNGQVIVKVNNG 1705

Qy        834 AGGSVTSITPKQSLCDGQWHSVAVSIKQRILHL 866
                ||:||||||||:|| : |     :: |
Db       1706 IRDFSTSVTPKQSLCDGRWHRITVIRDSNVVQL 1738


RESULT 15
US-09-561-818A-12
; Sequence 12, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
;  APPLICANT: Kortesmaa, Jarrko
;  APPLICANT:  Tryggvason, Karl
;  TITLE OF INVENTION: Laminin 8 and Methods For Its Use
;  FILE REFERENCE: 99,274-D
;  CURRENT APPLICATION NUMBER: US/09/561,818A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 1792
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-561-818A-12

  Query Match             26.3%;  Score 1183;  DB 4;  Length 1792;
  Best Local Similarity   32.7%;  Pred. No. 3.6e-108;
  Matches  304;  Conservative  165;  Mismatches  378;  Indels   82;  Gaps   26;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQ---RPDLRENGGTEDMFVMYLGNKDASKD 57
              | |:|:| |||     ::||| :||:||:::   :|          | ||:|||:|:| |:
Db        805 MMFDGQSAVEVHPKVSVDDLKAFTSISLYMKPPPKPAEPTGAWVADQFVLYLGSKNAKKE 864

Qy         58 YIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEA 117
              |:|:|: :  |  ||||| :: |: :|       |  |    || :|: :  |:  |  :
Db        865 YMGLAIKNDNLVYVYNLGMKDVEILLDS--KPVSSWPAYFSIVKIERVGEHGKVFLTVPS 922

Qy        118 TSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDL 177
               |:  :   :   |    ::||:: ||| |||||| | :|:||: |  | | ||:||  |
Db        923 LSSTAEEKFIKKGEFAGDDSLLDVTPEDTVFYVGGVPANFKLPASLNLPSYSGCLELATL 982

Qy        178 NENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYA--RIPTQPN--AP 228
              | :|:|||||  :|:: ::  || | |       :  :|:|: ||  |  |:
Db        983 NNDVISLYNFKHIYNMDPSKSVPCARDKLAFTQSRAASYFFDGSSYAVVRDITRRGKFGQ 1042

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLN-SEPPKEKGIRDT---- 283
                |   |:|  | ||:    |   | || : :| | | |    |  |    : ||
Db       1043 VTRFDIEIRTPADNGLVLLMVNGSMFFSLEMRNGYLHVFYDFGFSNGPVH--LEDTLKKA 1100

Qy        284 -INDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIPIAIRERFNI 339
               ||| | | | | |     |:| : |: | |:    | :   |:  |:|| |  : :   :
Db       1101 QINDAKYHEISI-IYHNDKKMILVVDRRHVKSTDNEKKKIPFTDIYIGGAPQEVLQSRTL 1159

Qy        340 STPA-----FQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFT 391
                    |:||||     ||   ::   :|:||   | ||  : | | |:  ||
Db       1160 RAHLPLDINFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIA 1217

Qy        392 NLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSP 450
              ::  :   | |:  | |:| ||:| |  : : :    ::|::| : :  :   | :  :
Db       1218 SIQKISFFDGFEGGFNFRTLQPNGLLFYYTSGSDVFSISLDNGTVVMDVK--GIKVMSTD 1275

Qy        451 GTYMDGLLHH-VSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQQS------LRLGG---- 499
               | ||| |  |: ||||    |::|   ||      |:  |:|:          ||
Db       1276 KQYHDGLPHFVVTSISDTR-YELVVDKSRLRGKN--PTKGKAEQTQTTEKKFYFGGSPIS 1332

Qy        500 ---GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 556
                :| |||||    |  :  || |    | |   ||  | :   |  :| |  |  :|
Db       1333 PQYANFTGCISNAYFTRLDRDVEVEDFQRYSEKVHTSLYECPIESSPLFLLHKKGKNSSK 1392

Qy        557 GRIFNVNQLMQDAP-----------QATRSTEAWQDGRSCLPPLNTKASHRALQFGDSP 604
               :    :  :|||            :| | :         |    : :|   | |:| :
Db       1393 PKTNKQGEKSKDAPSWDPIGLKFLEQKAPRDSH-------CHLSSSPRAIEHAYQYGGTA 1445

Qy        605 TSHLLLKLPQELLKPRSQFSLDIQTTSPKGLVFYAGTKD--SFLALYVADGRVVFALGAG 662
              |    :  |     :|||:: ::| |  |::||   ::   |: |::| ||:||    |
Db       1446 NSRQEFEHEQGDFGEKSQFAIRLKTRSSHGMIFYVSDQEENDFMTLFLAHGRLVFMFNVG 1505

Qy        663 GKKLRLRSKERYHDGKWHTVVFGLNGGKARLVVDGLRAQEGSL-PGNSTISPREQVYL-G 720
              |||::||:|:|:|| || |:|       |||:|||  |  | |  :    :  :|| |
Db       1506 HKKLKIRSQEKYNDGLWHDVIFIREKSSGRLVIDGLRVLEERLPPSGAAWKIKGPIYLGG 1565

Qy        721 LPLSRKPKSL---PQHSFVGCLRDFQLNSKPLDSPSARFGVSPCLGGSLEKGIYFSQGGG 777
              :  |  |::    :|| ||| : |||   : | |  | |:||  | :| | |||  ||
Db       1566 VAPGRAVKNVQITSVYSFSGCLGNLQLNGASITSASQTFSVTPCFEGPMETGTYFSTEGG 1625

Qy        778 HVILANSVSLGPELKLTFSIRPRSLTGVLIHVGSQSGQRLSVYMEAGKVTTSVSSDAGGS 837
              :|:|  | ::| : :: | :|||| :| |:|  | :|: |:|:|  |:|  |::
Db       1626 YVVLDESFNIGLKFEIAFEVRPRSSSGTLVHGHSVNGEYLNVHMRNGQVIVKVNNGVRDF 1685

Qy        838 VTSITPKQSLCDGQWHSVAVSIKQRILHL 866
              ||:||||:||||:|| : |     :: |
Db       1686 STSVTPKQNLCDGRWHRITVIRDSNVVQL 1714


Search completed: February 22, 2005, 08:40:52
Job time : 44.4378 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:05:49 ; Search time 15.0758 Seconds
(without alignments)
3605.942 Million cell updates/sec

Title: US-10-817-423-4
Perfect score: 2940
Sequence: 1 MRFNGKSGVEVRLPNDLEDL.....MLFKSPKRFNKGRIFNVNQL 565

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2439	83.0	1713	2	A55347	adhesive ligand ep
2	686	23.3	1816	1	S68960	laminin alpha-4 ch
3	681	23.2	3635	2	T10053	laminin alpha 5 ch
4	395	13.4	3712	2	S18253	laminin alpha-1 ch
5	302	10.3	3106	1	S53868	laminin alpha-2 ch
6	298.5	10.2	3672	2	T23433	hypothetical prote
7	298.5	10.2	3704	2	T37316	probable laminin a
8	294	10.0	1751	1	MMHUMH	laminin alpha-2 ch
9	280	9.5	3084	1	MMMSA	laminin alpha-1 ch
10	270	9.2	3075	2	S14458	laminin alpha-1 ch
11	247	8.4	3102	2	T43291	laminin alpha chai
12	222.5	7.6	2823	2	F87908	protein T22A3.8 [i
13	222.5	7.6	2823	2	T23064	hypothetical prote
14	212.5	7.2	1438	2	A48216	neurexin III-alpha
15	212.5	7.2	1471	2	B48218	neurexin III-alpha
16	212.5	7.2	1578	2	I48216	neurexin III-alpha
17	199.5	6.8	1530	2	I45944	neurexin I-alpha -
18	199	6.8	1507	2	A40228	neurexin I-alpha p
19	175	6.0	1715	2	C40228	neurexin II-alpha
20	170	5.8	1283	2	T13799	neurexin IV - frui
21	160.5	5.5	1264	2	T19545	hypothetical prote
22	159	5.4	3707	2	S18252	heparan sulfate pr
23	153	5.2	4391	2	A38096	perlecan precursor
24	147.5	5.0	281	2	T33466	hypothetical prote
25	143.5	4.9	1955	1	AGCH	agrin precursor -
26	142	4.8	1523	2	T13953	MEGF5 protein - ra
27	140	4.8	2610	2	T20968	hypothetical prote
28	138.5	4.7	1381	2	T31083	paranodin - rat
29	138	4.7	1025	2	T42626	secreted leucine-r
30	137.5	4.7	1385	2	T14158	neurexin IV - mous
31	135.5	4.6	1328	2	T43060	agrin - electric r
32	128.5	4.4	3034	2	T14119	seven-pass transme
33	128	4.4	637	2	F83939	myo-inositol catab
34	128	4.4	1531	2	T42218	slit-1 protein hom
35	125	4.3	403	2	A26371	sex steroid-bindin
36	124.5	4.2	601	2	T22025	hypothetical prote
37	124.5	4.2	601	2	D89711	protein F40E10.4 [
38	124.5	4.2	673	2	A48089	growth arrest-spec
39	122	4.1	2325	2	A61208	chondroitin sulfat
40	121.5	4.1	935	2	A64608	excinuclease ABC c
41	121.5	4.1	2809	2	T30213	G-cadherin - sea u
42	120	4.1	757	2	T34362	hypothetical prote
43	120	4.1	768	2	B97725	outer membrane pro
44	119.5	4.1	627	2	A41609	dnaK-type molecula
45	119.5	4.1	1417	2	AG2137	hypothetical prote

ALIGNMENTS

RESULT 1
A55347
adhesive ligand epiligrin, alpha-3 chain form A precursor - human
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C;Accession: A55347
R;Ryan, M.C.; Tizard, R.; VanDevanter, D.R.; Carter, W.G.
J. Biol. Chem. 269, 22779-22787, 1994
A;Title: Cloning of the LamA3 gene encoding the alpha3 chain of the adhesive ligand epi
A;Reference number: A55347; MUID:94357926; PMID:8077230
A;Accession: A55347
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1713 <RYA>
A;Cross-references: UNIPROT:Q16787; GB:L34155; NID:g551596; PID:g551597
C;Superfamily: laminin alpha-4 chain; laminin G repeat homology; laminin-type EGF-like
C;Keywords: alternative splicing
F;67-114/Domain: laminin-type EGF-like homology <LE2>
F;1392-1534/Domain: laminin G repeat homology <LG4>

Query Match 83.0%; Score 2439; DB 2; Length 1713;
Best Local Similarity 81.9%; Pred. No. 5.9e-165;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||: ||||||:||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :||||||||||: ||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNPKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNPKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||||||:|||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||:||||||||:|||:| :| || | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190
```

```
Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQL 1335
```

RESULT 2
S68960
laminin alpha-4 chain precursor - human
N;Alternate names: laminin Ah
C;Species: Homo sapiens (man)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: S68960; S65926; S49149; S40150; I53516
R;Richards, A.; Al-Imara, L.; Pope, F.M.
Eur. J. Biochem. 238, 813-821, 1996
A;Title: The complete cDNA sequence of laminin alpha-4 and its relationship to the other
A;Reference number: S68960; MUID:96300249; PMID:8706685
A;Accession: S68960
A;Molecule type: mRNA
A;Residues: 1-1816 <RIC>
A;Cross-references: UNIPROT:Q16363; UNIPROT:Q14731; EMBL:X91171; NID:g1212962; PIDN:CAA6
A;Experimental source: tissue type heart
R;Iivanainen, A.; Sainio, K.; Sariola, H.; Tryggvason, K.
FEBS Lett. 365, 183-188, 1995
A;Title: Primary structure and expression of a novel human laminin alpha-4 chain.
A;Reference number: I53516; MUID:95300971; PMID:7781776
A;Accession: S65926
A;Molecule type: mRNA
A;Residues: 1-142,'P',144-177,'F',179-490,'Y',492-1056,'P',1058-1816 <IIV>
A;Cross-references: EMBL:S78569; NID:g1042081; PIDN:AAB34635.1; PID:g1042082
R;Richards, A.J.; Al-Imara, L.; Carter, N.; Leversha, M.; Lloyd, J.C.; Pope, F.M.
submitted to the EMBL Data Library, December 1993
A;Description: Localisation of the gene (LAMA4) to chromosome 6q21 and isolation of a pa
A;Reference number: S49149
A;Accession: S49149
A;Molecule type: mRNA
A;Residues: 236-1816 <RI2>
A;Cross-references: EMBL:X76939; NID:g509805; PIDN:CAA54258.1; PID:g509806
R;Richards, A.J.; Al-Imara, L.; Carter, N.; Lloyd, J.C.; Pope, F.M.
submitted to the EMBL Data Library, February 1993
A;Description: Isolation of a partial cDNA encoding a protein homologous to laminin A. A
A;Reference number: S40150
A;Accession: S40150
A;Molecule type: mRNA
A;Residues: 1403-1541,'S',1543-1816 <RI3>
A;Cross-references: EMBL:X70904; NID:g437804; PIDN:CAA50261.1; PID:g437805
C;Genetics:
A;Gene: GDB:LAMA4; LAMA3
A;Cross-references: GDB:203904; OMIM:600133
A;Map position: 6q21-6q21
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin alpha-4 chain; laminin G repeat homology; laminin-type EGF-like h
C;Keywords: basement membrane; cell binding; coiled coil; extracellular matrix; glycoprc
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-1816/Product: laminin alpha-4 chain #status predicted <MAT>
F;82-129/Domain: laminin-type EGF-like homology <LE1>
F;132-184/Domain: laminin-type EGF-like homology <LE2>
F;187-238/Domain: laminin-type EGF-like homology <LE3>
F;241-265/Domain: laminin-type EGF-like homology #status atypical <LE4>
F;717-719/Region: cell attachment (R-G-D) motif
F;862-1031/Domain: laminin G repeat homology <LG1>
F;1068-1223/Domain: laminin G repeat homology <LG2>
F;1252-1398/Domain: laminin G repeat homology <LG3>
F;1488-1636/Domain: laminin G repeat homology <LG4>
F;1665-1816/Domain: laminin G repeat homology <LG5>
F;104,215,308,458,524,550,571,574,631,639,735,751,754,780,803,1086,1281,1359,1411/Bindir
F;266,269/Disulfide bonds: interchain #status predicted

```
  Query Match             23.3%;  Score 686;  DB 1;  Length 1816;
  Best Local Similarity   32.2%;  Pred. No. 3.7e-40;
  Matches  194;  Conservative  101;  Mismatches  245;  Indels   62;  Gaps   21;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFL----QRPDLRENGGTEDMFVMYLGNKDASK 56
              | |:|:| |||      ::||| :|||||::    :||:| |   | | |::|||:|:| |
Db        829 MMFDGQSAVEVHSRTSMDDLKAFTSLSLYMKPPVKRPELTE---TADQFILYLGSKNAKK 885

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
              :|:|:|: :  |  ||||| :: |: :|       |  |     || :|: :  |:  |
Db        886 EYMGLAIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVP 943

Qy        117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDD 176
              : |:  :   :   |    ::||:||||| |||||| | :|:||: |  | : ||:||
Db        944 SLSSTAEEKFIKKGEFSGDDSLLDLDPEDTVFYVGGVPSNFKLPTSLNLPGFVGCLELAT 1003

Qy        177 LNENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYA--RIPTQPN--A 227
              || :|:|||||  :|:: :   || | |       :  :|:|:|||  |  |:
Db       1004 LNNDVISLYNFKHIYNMDPSTSVPCARDKLAFTQSRAASYFFDGSGYAVVRDITRRGKFG 1063

Qy        228 PFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRY-------KLNSEPPKEKGI 280
                |   ::|  | ||:    |   |  | : :| | | |       ::: |   :|
Db       1064 QVTRFDIEVRTPADNGLILLMVNGSMFFRLEMRNGYLHVFYDFGFSSGRVHLEDTLKKA- 1122

Qy        281 RDTINDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIP------I 331
              ||| | | | | |    |:| : |: | |:    |      |:  |:|| |
Db       1123 --QINDAKYHEISI-IYHNDKKMILVVDRRHVKSMDNEKMKIPFTDIYIGGAPPEILQSR 1179

Qy        332 AIRERFNISTPAFQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQM 388
              |:|    :    |:|||      ||   ::   :|:||   | ||  : | | |:  ||
Db       1180 ALRAHLPLDI-NFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQS 1236

Qy        389 SFTNLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIF 447
              ::  :   | |:  | |:| ||:| |  : : :    ::|::| : :  :   | :
Db       1237 FIASIQKISFFDGFEGGFNFRTLQPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQ 1294

Qy        448 KSPGTYMDGLLHHVSVISDTSGLR--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-- 499
                | ||| |   |||  |  |  |::|  :|  :|          | | :    ||
Db       1295 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSP 1352

Qy        500 -----GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
                  :| |||||    |  :  || |    : |   ||  | :   |  :| |  |
Db       1353 ISAQYANFTGCISNAYFTRVDRDVEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNL 1412

Qy        555 NK 556
              :|
Db       1413 SK 1414
```

RESULT 3
T10053
laminin alpha 5 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10053
R;Miner, J.H.; Lewis, R.M.; Sanes, J.R.
submitted to the EMBL Data Library, November 1997
A;Reference number: Z16923
A;Accession: T10053
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3635 <MIN>
A;Cross-references: UNIPROT:Q61001; EMBL:U37501; NID:g2599231; PID:g2599232
C;Genetics:
A;Gene: Lama5
C;Keywords: basement membrane; cell binding; extracellular matrix
F;1888-1939/Domain: laminin-type EGF-like homology <LEG>
F;1942-1970/Domain: EGF homology <EGF>

```
  Query Match           23.2%;  Score 681;  DB 2;  Length 3635;
  Best Local Similarity   31.8%;  Pred. No. 2.4e-39;
  Matches  186;  Conservative  111;  Mismatches  210;  Indels   78;  Gaps   22;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGG--TEDMFVMYLGNKDASKDY 58
              |:|||:||| :| | || ||  ||:|   :| |      |  | | ||:|:|:: |: ||
Db       2656 MKFNGRSGVRLRPPRDLADLAAYTALKFHIQSPVPAPEPGKNTGDHFVLYMGSRQATGDY 2715

Qy         59 IGMAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEA 117
              :|::: : ::  || ||      : ||: : |         |   |  ||  :: | |
Db       2716 MGVSLRNQKVHWVYRLGKAGPTTLSIDENIGEQ------FAAVSIDRTLQFGHMSVTVE- 2768

Qy        118 TSNKPKAPAVYDLEGGS----SNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIE 173
                      |::::| :    |  |||| |:| |||||||| :|  |  |||| | ||||
Db       2769 ------KQMVHEIKGDTVAPGSEGLLNLHPDDFVFYVGGYPSNFTPPEPLRFPGYLGCIE 2822

Qy        174 LDDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPNAP 228
              :: ||| |:|||||: || |:|   :|| | |       :| :| :|:|:||| :
Db       2823 METLNEEVVSLYNFEQTFMLDTAVDKPCARSKATGDPWLTDGSYLDGSGFARISFEKQ-- 2880

Qy        229 FPN---FIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPPK- 276
              | |   | | ::     |::|| : :  |: | :::| |:: |    |         :||:
Db       2881 FSNTKRFDQELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFGSGLKKADPLQPPQA 2940

Qy        277 ----EKGIRDTINDGKDHSILITIGKLQKRMWINVNERSVRIEGEIFDFSTYYLGGI--- 329
                  | |:  :  |    :|:   ::::    :|:: ::     |: |   |||||:
Db       2941 LTAASKAIQVFLLAGNRKRVLV---RVERATVFSVDQDNML---EMAD--AYYLGGVPPE 2992

Qy        330 --PIAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSR 384
                |:::|: |  |  : :||:| :|    |  : ||| | |::  |: |  : || :|
Db       2993 QLPLSLRQLFP-SGGSVRGCIKGIKALGKYVDLKRLN-TTGISFGCTADLLVGRTMTFHG 3050

Qy        385 GGQMSFTNLDV-PSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSN 443
              | :     || | |:     |||:  | :  |     :       |:| :||: |   :
Db       3051 HGFLPLALPDVAPITEVVYSGFGFRGTQDNNLLYYRTSPDGPYQVSLREGHVTLRFMNQE 3110

Qy        444 IPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDD--QVLRRNQRLPSFSNAQ----QSLRL 497
              :   ::   : ||  |:|:  |: :|: | :||  |::: ::|       |      | |
Db       3111 V---ETQRVFADGAPHYVAFYSNVTGVWLYVDDQLQLVKSHERTTPMLQLQPEEPSRLLL 3167

Qy        498 GG-------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLG 535
              ||        :| |||||| |||      | ||       : |:|
Db       3168 GGLPVSGTFHNFSGCISNVFVQRLRGPQRVFDLHQNMGSVNVSVG 3212


RESULT 4
S18253
laminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C;Accession: S28399; S18253
R;Kusche-Gullberg, M.; Garrison, K.; MacKrell, A.J.; Fessler, L.I.; Fessler, J.H.
EMBO J. 11, 4519-4527, 1992
A;Title: Laminin A chain: expression during Drosophila development and genomic sequence.
A;Reference number: S28399; MUID:93049203; PMID:1425586
A;Accession: S28399
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-3712 <KUS>
A;Cross-references: UNIPROT:Q00174; GB:M96388; NID:g157799; PIDN:AAA28662.1; PID:g157800
R;Garrison, K.; MacKrell, A.J.; Fessler, J.H.
J. Biol. Chem. 266, 22899-22904, 1991
A;Title: Drosophila laminin A chain sequence, interspecies comparison, and domain struct
A;Reference number: S18253; MUID:92078147; PMID:1744083
A;Accession: S18253
A;Molecule type: mRNA
A;Residues: 1762-3712 <GAR>
A;Cross-references: EMBL:M75882; NID:g157797; PIDN:AAA28661.1; PID:g157798
C;Genetics:
A;Gene: FlyBase:LanA
A;Cross-references: FlyBase:FBgn0002526
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C;Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular

F;273-330/Domain: laminin-type EGF-like homology <LEG>
F;333-400/Domain: laminin-type EGF-like homology <LE02>
F;541-584/Domain: laminin-type EGF-like homology <LEG1>
F;1776-2115/Domain: III <DOM3>
F;1776-1806/Domain: laminin-type EGF-like homology #status atypical <LE1>
F;1809-1856/Domain: laminin-type EGF-like homology <LE2>
F;1859-1914/Domain: laminin-type EGF-like homology <LE3>
F;1917-1967/Domain: laminin-type EGF-like homology <LE4>
F;1970-2014/Domain: laminin-type EGF-like homology <LE5>
F;2017-2061/Domain: laminin-type EGF-like homology <LE6>
F;2064-2109/Domain: laminin-type EGF-like homology <LE7>
F;2116-2697/Domain: I/II, heptad repeats <DOM2>
F;2698-3712/Domain: G <DOMG>
F;2698-2863/Domain: repeat G1 <RG1>
F;2864-3048/Domain: repeat G2 <RG2>
F;3049-3223/Domain: repeat G3 <RG3>
F;3079-3200/Domain: laminin G repeat homology <LG3>
F;3334-3528/Domain: repeat G4 <RG4>
F;3529-3712/Domain: repeat G5 <RG5>
F;1847,1850,1943,2024,2196,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2890,2938,

  Query Match           13.4%;  Score 395;  DB 2;  Length 3712;
  Best Local Similarity   25.5%;  Pred. No. 5.6e-19;
  Matches  155;  Conservative  105;  Mismatches  238;  Indels  110;  Gaps   27;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLG--NKDASK-- 56
              : |   : :|:: |   : |   |:|| : :     |  |    |::|||  || | |
Db       2675 VNFKPSTILELKTPEKTKLLATRTNLSTYFR---TTEPSG----FLLYLGNDNKTAQKNN 2727

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
              |:: : :|:|      :||:    :  |: : :    :||:||:        |||   :|
Db       2728 DFVAVEIVNGYPILTIDLGNGPERITSDKYVADGRWYQAVVDRMG-----PNAKLTIREE 2782

Qy        117 ATSNKPKAPAVYDLEGG---SSNTLLNLDPEDAVFYVGGYP--PDFELPSRLRFPPYKGC 171
                    |    |  : |    |  :|::|    :| |||||   ||  | |    : |
Db       2783 L----PNGDVVEHSKSGYLEGSQNILHVDKNSRLF-VGGYPGISDFNAPPDLTTNSFSGD 2837

Qy        172 IELDDLNENVLSLYNF--KTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPF 229
              ||   : :  : |:||       :    | :    :|:       |:| || ::    |
Db       2838 IEDLKIGDESVGLWNFVYGDDNDQGARERDVLLEKKKPVTGLRFKGNGYVQLNATSNLKS 2897

Qy        230 PNFIQ---TIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTIND 286
              : ||          |||||     :::|: : || :      |       : | :|  ||
Db       2898 RSSIQFSFKADKDTSNGLLFFYGRDKHYMSIEMIDGAIFFNISLGEGGGVQSGSQDRYND 2957

Qy        287 GKDHSI---------LITIGKLQKRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERF 337
              : | :          |: :    |:     :  : |:       | || |      |
Db       2958 NQWHKVQAERENRNGLLKVDDIV----ISRTNAPLEADLELPKLRRLYFGGHP----RRL 3009

Qy        338 NIS---TPAFQGCMKNLKKTSGVVRLNDTV---GVTKKCSEDWKLVRTASFSRGGQMSFT 391
              | |     | | ||: |:    ||| | : |   || : ||  :  | : :     | :
Db       3010 NTSISLQPNFDGCIDNVVINQGVVDLTEYVTGGGVEEGCSAKFSTVVSYAPHEYGFLRMN 3069

Qy        392 NLDVPSTDRFQLSFGFQTFQPSGTLL---NHQTRTSSLLVTLEDGHIELSTRDSNIPIFK 448
              |  | | :    :    |:| ||:| |     ||  ::|:: ::|:|| ::|::  | : |
Db       3070 N--VSSDNNLHVVLHFKTTQPNGVLFYAANHD-QSSTIGLSLQDGLLKLNSMGSQLVI-- 3124

Qy        449 SPGTYMDGLLH----HVSVISDTSG-LRLLIDDQVLRRNQRLPSFSNAQQSLRLGGG--- 500
                  | :|:    ||  :  | | ||| :||     |:|| |      | | | ||
Db       3125 -----DDRILNDGEDHVVTVQHTQGELRLTVDDV---DNKRLGS----PQPLILEGGDIF 3172

Qy        501 ------------------HFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNK 541
                              :| ||||:| |     : |::: |: : ||: :: ||
Db       3173 FAGLPDNYRTPRNALASLAYFVGCISDVTV-----NEEIINFANSAEKKNGNINGC---- 3223

Qy        542 PPFLMLFK 549
              || :: ::
Db       3224 PPHVLAYE 3231


RESULT 5
S53868
laminin alpha-2 chain precursor - mouse
```

```
N;Alternate names: laminin M chain; merosin heavy chain
C;Species: Mus musculus (house mouse)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: I49077; S50829; I48655; S31576; S53868
R;Bernier, S.M.; Utani, A.; Sugiyama, S.; Doi, T.; Polistina, C.; Yamada, Y.
Matrix Biol. 14, 447-455, 1995
A;Title: Cloning and expression of laminin alpha 2 chain (M-chain) in the mouse.
A;Reference number: I49077; MUID:95316259; PMID:7795883
A;Accession: I49077
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3106 <RES>
A;Cross-references: UNIPROT:Q60675; EMBL:U12147; NID:g699109; PIDN:AAC52165.1; PID:g6991
R;Xu, H.; Wu, X.R.; Wewer, U.M.; Engvall, E.
Nature Genet. 8, 297-302, 1994
A;Title: Murine muscular dystrophy caused by a mutation in the laminin alpha-2 (Lama2) g
A;Reference number: S50829; MUID:95179178; PMID:7874173
A;Accession: S50829
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 64-281 <XUH>
A;Cross-references: GB:S75315; NID:g833929; PIDN:AAB33573.1; PID:g833930
R;Chang, A.C.; Wadsworth, S.; Coligan, J.E.
J. Immunol. 151, 1789-1801, 1993
A;Title: Expression of merosin in the thymus and its interaction with thymocytes.
A;Reference number: I48655; MUID:93346725; PMID:8345183
A;Accession: I48655
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 2162-2204,'D',2206-2213,'EY',2216-2279 <RE2>
A;Cross-references: EMBL:X69869; NID:g53055; PIDN:CAA49502.1; PID:g53056
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C;Keywords: basement membrane; calcium binding; coiled coil; extracellular matrix; glycc
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-3106/Product: laminin alpha-2 chain #status predicted <MAT>
F;283-337/Domain: laminin-type EGF-like homology <LE01>
F;340-407/Domain: laminin-type EGF-like homology <LE02>
F;410-462/Domain: laminin-type EGF-like homology <LE03>
F;465-511/Domain: laminin-type EGF-like homology <LE04>
F;514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;720-750/Domain: laminin-type EGF-like homology <LE06>
F;753-800/Domain: laminin-type EGF-like homology <LE07>
F;803-858/Domain: laminin-type EGF-like homology <LE08>
F;861-911/Domain: laminin-type EGF-like homology <LE09>
F;914-960/Domain: laminin-type EGF-like homology <LE10>
F;963-1007/Domain: laminin-type EGF-like homology <LE11>
F;1010-1053/Domain: laminin-type EGF-like homology <LE12>
F;1056-1099/Domain: laminin-type EGF-like homology <LE13>
F;1102-1121/Domain: laminin-type EGF-like homology #status atypical <LE14>
F;1123-1159/Domain: laminin-type EGF-like homology #status atypical <LE15>
F;1162-1171/Domain: laminin-type EGF-like homology #status atypical <LE16>
F;1376-1413/Domain: laminin-type EGF-like homology #status atypical <LE17>
F;1416-1462/Domain: laminin-type EGF-like homology <LE18>
F;1465-1520/Domain: laminin-type EGF-like homology <LE19>
F;1523-1567/Domain: laminin-type EGF-like homology <LE20>
F;2166-2327/Domain: laminin G repeat homology <LG1>
F;2360-2520/Domain: laminin G repeat homology <LG2>
F;2546-2709/Domain: laminin G repeat homology <LG3>
F;2785-2933/Domain: laminin G repeat homology <LG4>
F;2960-3106/Domain: laminin G repeat homology <LG5>

  Query Match             10.3%;  Score 302;  DB 1;  Length 3106;
  Best Local Similarity   22.1%;  Pred. No. 1.8e-12;
  Matches  131;  Conservative  116;  Mismatches  227;  Indels  120;  Gaps   30;

Qy          32 RPDLRENG----------GTEDMFVMYLGNKDASK--DYIGMAVVDGQLTCVYNLGDREA 79
               ||::::                |  : |||   ::|  |:: : :  |::: :: :|
Db        2155 RPEIKKGSYNNIVVHVKTAVADNLLFYLG---SAKFIDFLAIEMRKGKVSFLWIVGSGVG 2211

Qy          80 EVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSNKPKA---PAVYDLEGGSSN 136
                |    :  :    ::   |:: |  :   ::       : |||   |: |
Db        2212 RVGFPDLTID----DSYWYRIEASRTGRNGSISV---RALDGPKASMVPSTYHSVSPPGY 2264

Qy         137 TLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNENVLSLYNFKTTFNLNTT 196
               |:|::|  :|: :|||     :    :|  : ||:     :   : |:||:
Db        2265 TILDVD-ANAMLFVGGLTGKIKKADAVRVITFTGCMGETYFDNKPIGLWNFRE----KEG 2319

Qy         197 EVEPCRRRKEESDKN---YFEGTGYARIPTQPNAPFPNFIQTI----QTTVDRGLLFFAE 249
               : : |    :  |       |:| ||| : ::|   :|| | |:    :|     || :
Db        2320 DCKGCTVSPQVEDSEGTIQFDGEGYALV-SRPIRWYPN-ISTVMFKFRTFSSSALLMYLA 2377

Qy         250 NQD--NFISLNIEDGNLMVRYKLNSEPPKEKGIRDTI-----NDGKDHSILITIGKLQKR 302
               :|  :|:|: : ||:: | | | |      |:  :     ||||  :   |: ::||:
Db        2378 TRDLKDFMSVELSDGHVKVSYDLGS------GMTSVVSNQNHNDGKWKA--FTLSRIQKQ 2429

Qy         303 MWINV------NERSVRIEGEIFDF-------STYYLGGIP----IAIRERFNISTPAFQ 345
                 |::       | :|       :|          | ||:|    :::: |  ::   :
Db        2430 ANISIVDIDSNQEENVATSSSGNNFGLDLKADDKIYFGGLPTLRNLSMKARPEVNVKKYS 2489

Qy         346 GCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGG--QMSFTNLDVPSTDR 400
               ||:|::   :    ::   | ||||| ||   : | | || : |  :::  ::|| :
Db        2490 GCLKDIEISRTPYNILSSPDYVGVTKGCS--LENVNTVSFPKPGFVELAAVSIDVGT--- 2544

Qy         401 FQLSFGFQTFQPSGTLL------------NHQTRTSSLLVTLEDG----HIELSTRD-S 442
                :::  | |   || :|             ||  :   : | |    |:   ||
Db        2545 -EINLSFSTRNESGIILLGSGGTLTPPRRKRRQTTQAYYAIFLNKGRLEVHLSSGTRTMR 2603

Qy         443 NIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQ-QSLRLGGG- 500
               | |   |  : || | | |   | |:  :  |:  | | |       : : | :||
Db        2604 KIVIKPEPNLFHDGREHSVHV-ERTRGIFTVQIDEDRRHIQNLTEEQPIEVKKLFVGGAP 2662

Qy         501 -----------HFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKP 542
                          |:|: |:::         :| |     |:| :| |:  ||
Db        2663 PEFQPSPLRNIPAFQGCVWNLVINSIP-----MDFAQPIAFKNADIGRCTYQKP 2711


RESULT 6
T23433
hypothetical protein K08C7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23433
R;Berks, M.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19740
A;Accession: T23433
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3672 <WIL>
A;Cross-references: UNIPROT:Q21313; EMBL:Z70286; PIDN:CAA94293.1; GSPDB:GN00022; CESP:K0
A;Experimental source: clone K08C7
C;Genetics:
A;Gene: CESP:K08C7.3
A;Map position: 4
A;Introns: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 3
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

  Query Match             10.2%;  Score 298.5;  DB 2;  Length 3672;
  Best Local Similarity   23.5%;  Pred. No. 4.1e-12;
  Matches  141;  Conservative  106;  Mismatches  233;  Indels  121;  Gaps   27;

Qy           3 FNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDA-------- 54
                 |   | ::: :|  :      :  :| : :    :|:|       :: ||::
Db        2696 FEKGSSLDLNIPQRVTRSAAHADISFYFRTE--QEHG-----IPLFFGNEETAVGSRAVP 2748

Qy          55 SKDYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYT 114
               : ||:   :  |:    :|||  | |::|     :  : :  |:  :||        |
Db        2749 TADYVAAEIEYGRPKITVDLGDAPAVVKLD-----TPVNDGLWRRLNIERI------GKT 2797

Qy         115 KEATSNKPKAPAVYDLE---GGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGC 171
               | :|| :    : :    | : ::|||: : :  :||| |    :   |    : |
Db        2798 VSVTLSKPNSVETAETKSSVAGGNKSVLNLNQQISRLFVGGVPTSARISKDLYNRDFVGD 2857
```

```
Qy       172 IELDDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNY--FEGTGYA---------R 220
Db      2858 IESLKLHGEPIGLWNSREKGNTNVNGAQKKPKITDNADELVVSLDGEGYTSYKPSHWNPR 2917

Qy       221 IPTQPNAPFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGI 280
Db      2918 KATKISLSFLTF-------SPHGLLFFVGKDKDFMALELSDGGVKLSVDLGS------GV 2964

Qy       281 RDTI------NDGKDHSILITIGKLQKRMWINVNERSVRIEGEI----FDFST---YYLG 327
Db      2965 GQWITESSNYNDGKWHT--VSIVREEKHVKIMIDGETEVLEGDVPGKDSEMSVTEFLYIG 3022

Qy       328 GIPIAIRERFNISTPAFQGCMKNLKKTSGVVRLND---TVGVTKKCSEDWKLVRTASF-S 383
Db      3023 GTPSGLSVRTTI--VPLRGCIKSVKLGSDNVDLESSHASKGVRSGC--PLHSVRTVSFLS 3078

Qy       384 RGGQMSFTNLDVPSTDRFQLSFGFQT---FQPSGTLLNHQTRTSSLLVTL-EDGHIELST 439
Db      3079 DRTTASFNNATEFSED-VSVTFKFKTRSIRQPSSLFTVNDDEDSVLSVSINEDGILTVTS 3137

Qy       440 RD--SNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQQSLRL 497
Db      3138 GEDIATLELAASP----DEKWHYVSIRKTKYIIRIDADD----------SFSNEVARKHA 3183

Qy       498 GGGH-----------------FEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSL 539
Db      3184 DDSNPDASFLSAFFGKSGETPSFVGCIGDVTL-----NGKLLDFAN-SEIKEISLNGCSL 3237

Qy       540 N 540
Db      3238 S 3238
```

RESULT 7
T37316
probable laminin alpha chain - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37316
R;Joh, K.; Zhu, K.; Hedgecock, E.M.; Inoue, T.; Hori, K.
submitted to the EMBL Data Library, August 1998
A;Description: Laminin alpha chain gene in the nematode C. elegans.
A;Reference number: Z21681
A;Accession: T37316
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3704 <JOH>
A;Cross-references: UNIPROT:P91904; EMBL:AB016806; PIDN:BAA32347.1
A;Experimental source: strain N2
C;Genetics:
A;Gene: epi-1
A;Map position: IV
A;Introns: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 3
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

  Query Match   10.2%; Score 298.5; DB 2; Length 3704;
  Best Local Similarity   23.5%; Pred. No. 4.1e-12;
  Matches 141; Conservative 106; Mismatches 233; Indels 121; Gaps   27;

```
Qy         3 FNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDA-------- 54
Db      2696 FEKGSSLDLNIPQRVTRSAAHADISFYFRTE--QEHG-----IPLFFGNEETAVGSRAVP 2748

Qy        55 SKDYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYT 114
Db      2749 TADYVAAEIEYGRPKITVDLGDAPAVVKLD-----TPVNDGLWRRLNIERI------GKT 2797

Qy       115 KEATSNKPKAPAVYDLE---GGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGC 171
Db      2798 VSVTLSKPNSVETAETKSSVAGGNKSVLNLNQQISRLFVGGVPTSARISKDLYNRDFVGD 2857

Qy       172 IELDDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNY--FEGTGYA---------R 220
```

```
Db      2858 IESLKLHGEPIGLWNSREKGNTNVNGAQKKPKITDNADELVVSLDGEGYTSYKPSHWNPR 2917

Qy       221 IPTQPNAPFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGI 280
Db      2918 KATKISLSFLTF-------SPHGLLFFVGKDKDFMALELSDGGVKLSVDLGS------GV 2964

Qy       281 RDTI------NDGKDHSILITIGKLQKRMWINVNERSVRIEGEI----FDFST---YYLG 327
Db      2965 GQWITESSNYNDGKWHT--VSIVREEKHVKIMIDGETEVLEGDVPGKDSEMSVTEFLYIG 3022

Qy       328 GIPIAIRERFNISTPAFQGCMKNLKKTSGVVRLND---TVGVTKKCSEDWKLVRTASF-S 383
Db      3023 GTPSGLSVRTTI--VPLRGCIKSVKLGSDNVDLESSHASKGVRSGC--PLHSVRTVSFLS 3078

Qy       384 RGGQMSFTNLDVPSTDRFQLSFGFQT---FQPSGTLLNHQTRTSSLLVTL-EDGHIELST 439
Db      3079 DRTTASFNNATEFSED-VSVTFKFKTRSIRQPSSLFTVNDDEDSVLSVSINEDGILTVTS 3137

Qy       440 RD--SNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQQSLRL 497
Db      3138 GEDIATLELAASP----DEKWHYVSIRKTKYIIRIDADD----------SFSNEVARKHA 3183

Qy       498 GGGH-----------------FEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSL 539
Db      3184 DDSNPDASFLSAFFGKSGETPSFVGCIGDVTL-----NGKLLDFAN-SEIKEISLNGCSL 3237

Qy       540 N 540
Db      3238 S 3238
```

RESULT 8
MMHUMH
laminin alpha-2 chain - human (fragment)
N;Alternate names: laminin M chain; merosin heavy chain
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: PX0082; A35899; A38970; S14461
R;Hori, H.; Kanamori, T.; Mizuta, T.; Yamaguchi, N.; Liu, Y.; Nagai, Y.
J. Biochem. 116, 1212-1219, 1994
A;Title: Human laminin M chain: Epitope analysis of its monoclonal antibodies by immunc
A;Reference number: PX0082; MUID:95221315; PMID:7535762
A;Accession: PX0082
A;Molecule type: mRNA
A;Residues: 1-1751 <HOR>
A;Cross-references: UNIPROT:P24043
A;Experimental source: placenta
R;Ehrig, K.; Leivo, I.; Argraves, W.S.; Ruoslahti, E.; Engvall, E.
Proc. Natl. Acad. Sci. U.S.A. 87, 3264-3268, 1990
A;Title: Merosin, a tissue-specific basement membrane protein, is a laminin-like protei
A;Reference number: A35899; MUID:90238994; PMID:2185464
A;Accession: A35899
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 'V',623-1751 <EHR1>
A;Cross-references: EMBL:M59832
A;Accession: A38970
A;Molecule type: protein
A;Residues: 1368-1384;1389-1406;1593-1607 <EHR2>
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in lacking 1599-
R;Ehrig, K.; Leivo, I.; Argraves, S.W.; Ruoslahti, E.; Engvall, E.
submitted to the EMBL Data Library, December 1990
A;Description: The tissue-specific basement membrane protein merosin is a laminin-like
A;Reference number: S14461
A;Accession: S14461
A;Molecule type: mRNA
A;Residues: 'V',623-1264,'R',1266-1751 <LEI>
A;Cross-references: EMBL:M59832; NID:g187520; PIDN:AAA63215.1; PID:g187521
C;Comment: This protein is a prominent component of the basement membrane that mediates
C;Genetics:
A;Gene: GDB:LAMA2; LAMM
A;Cross-references: GDB:132362; OMIM:156225
A;Map position: 6q22-6q23
```
```

```
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C;Keywords: basement membrane; calcium binding; coiled coil; extracellular matrix; glycc
F;21-58/Domain: laminin-type EGF-like homology #status atypical <LE01>
F;61-107/Domain: laminin-type EGF-like homology <LE02>
F;110-165/Domain: laminin-type EGF-like homology <LE03>
F;168-212/Domain: laminin-type EGF-like homology <LE04>
F;527-567,1071-1300/Region: 3DM and 2D9 binding
F;811-972/Domain: laminin G repeat homology <LG1>
F;1005-1165/Domain: laminin G repeat homology <LG2>
F;1191-1354/Domain: laminin G repeat homology <LG3>
F;1430-1578/Domain: laminin G repeat homology <LG4>
F;1605-1751/Domain: laminin G repeat homology <LG5>
F;120,238,255,341,451,542,557,561,658,669,686,767,881,1001,1076,1119,1192,1199,1289,1509

  Query Match             10.0%;  Score 294;  DB 1;  Length 1751;
  Best Local Similarity   23.6%;  Pred. No. 2.8e-12;
  Matches  135;  Conservative  105;  Mismatches  221;  Indels  112;  Gaps   28;

Qy          43 DMFVMYLGNKDASK--DYIGMAVVDGQLTCVYNLGDREAEVQI-DQVLTESESQEAVMDR 99
               |  : |||   ::|  |:: : :  |::: ::::|     |:  |  : :|     |  |
Db         821 DNLLFYLG---SAKFIDFLAIEMRKGKVSFLWDVGSGVGRVEYPDLTIDDSYWYRIVASR 877

Qy         100 VKFQRIYQFAKLNYTKEATSNKPKA---PAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPD 156
                         |         : |||    |: :         |:|::|  :|: :|||
Db         878 TGRNGTISVRAL--------DGPKASIVPSTHHSTSPPGYTILDVD-ANAMLFVGGLTGK 928

Qy         157 FELPSRLRFPPYKGCIELDDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKN---YF 213
                :    :|   : ||:      :   : |:||:         : : |    :  |      |
Db         929 LKKADAVRVITFTGCMGETYFDNKPIGLWNFRE----KEGDCKGCTVSPQVEDSEGTIQF 984

Qy         214 EGTGYARIPTQPNAPFPNFIQTI----QTTVDRGLLFFAENQD--NFISLNIEDGNLMVR 267
               :| ||| : ::|   :|| | |:    :|     || :   :|  :|:|: : ||:: |
Db         985 DGEGYALV-SRPIRWYPN-ISTVMFKFRTFSSSALLMYLATRDLRDFMSVELTDGHIKVS 1042

Qy         268 YKLNSEPPKEKGIRDTI-----NDGKDHSILITIGKLQKRMWINVNERSVRIEGEIFDFS 322
               | | |       |:   :     ||||  |   |: ::||:  |:: :     |  |   |
Db        1043 YDLGS------GMASVVSNQNHNDGKWKS--FTLSRIQKQANISIVDIDTNQEENIATSS 1094

Qy         323 T-------------YYLGGIP----IAIRERFNISTPAFQGCMKNL---KKTSGVVRLND 362
               :              | ||:|    :::: |  ::   : ||:|::   :    ::   |
Db        1095 SGNNFGLDLKADDKIYFGGLPTLRNLSMKARPEVNLKKYSGCLKDIEISRTPYNILSSPD 1154

Qy         363 TVGVTKKCSEDWKLVRTASFSRGG--QMSFTNLDVPSTDRFQLSFGFQTFQPSGTLL--- 417
               |||||  ||   : | | || : |  ::|   :|| :    :::  | |   || :|
Db        1155 YVGVTKGCS--LENVYTVSPPKPGFVELSPVPIDVGT----EINLSFSTKNESGIILLGS 1208

Qy         418 ----------NHQTRTSSLLVTLEDGHIE--LST---RDSNIPIFKSPGTYMDGLLHHVS 462
                         ||   :  :: |  | :|  |||       | |   |  : ||  | |
Db        1209 GGTPAPPRRKRRQTGQAYYVILLNRGRLEVHLSTGARTMRKIVIRPEPNLFHDGREHSVH 1268

Qy         463 VISDTSGLRLLIDDQVLRRNQRLPSFSNAQ-QSLRLGGG-------------HFEGCISN 508
               |   | |:  :  |:  |  | |       : : | :||             |||| |
Db        1269 V-ERTRGIFTVQVDENRRYMQNLTVEQPIEVKKLFVGGAPPEFQPSPLRNIPPFEGCIWN 1327

Qy         509 VLVQRFSQSPEVLDLASKSTKKDASLGGCSLNK 541
               :::          :| |   : |:| :| |:  |
Db        1328 LVINSVP-----MDFARPVSFKNADIGRCAHQK 1355


RESULT 9
MMMSA
laminin alpha-1 chain precursor - mouse
N;Alternate names: laminin chain A1
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: A31771; A30449; S00624; A30450; S08895; S02678; S01790; A30451; S14670
R;Sasaki, M.; Kleinman, H.K.; Huber, H.; Deutzmann, R.; Yamada, Y.
J. Biol. Chem. 263, 16536-16544, 1988
A;Title: Laminin, a multidomain protein. The A chain has a unique globular domain and ho
A;Reference number: A31771; MUID:89034134; PMID:3182802
A;Accession: A31771
A;Molecule type: mRNA
A;Residues: 1-3084 <SAS>
A;Cross-references: UNIPROT:P19137; EMBL:J04064; NID:g309419; PIDN:AAA39410.1; PID:g3094
A;Accession: A30449
A;Molecule type: protein
A;Residues: 183-195;570-571,'A',573-586;596-612,'X',614-617,'EMK';630-646;1217-1222,'YPF
2486;2624-2639;2818-2843;3009-3033,'V',3035 <SA2>
R;Hartl, L.; Oberbaeumer, I.; Deutzmann, R.
Eur. J. Biochem. 173, 629-635, 1988
A;Title: The N terminus of laminin A chain is homologous to the B chains.
A;Reference number: S00624; MUID:88225080; PMID:3267223
A;Accession: S00624
A;Molecule type: mRNA
A;Residues: 1-208,'T',210-334 <HAR>
A;Cross-references: EMBL:X07737; NID:g52857; PIDN:CAA30561.1; PID:g52858
A;Accession: A30450
A;Molecule type: protein
A;Residues: 311-335,'N',337-339;630-642,'D',644;692-734;737-748,'X',750-760,'G',762-763;
3-1389;1449-1459 <HA2>
A;Note: the sequence from Fig. 7 is inconsistent with that from Fig. 5 in having 209-Ile
R;Mann, K.; Deutzmann, R.; Timpl, R.
Eur. J. Biochem. 178, 71-80, 1988
A;Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th
A;Reference number: S08895; MUID:89078415; PMID:2462498
A;Accession: S08895
A;Molecule type: protein
A;Residues: 153-169 <MAN>
R;Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.
Biochem. J. 252, 453-461, 1988
A;Title: Structure and distribution of N-linked oligosaccharide chains on various domain
A;Reference number: S02678; MUID:88326259; PMID:2458101
A;Accession: S02678
A;Molecule type: protein
A;Residues: 630-642,'D',644;2690-2704 <FUJ>
R;Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaeumer, I.; Hartl, L.
Eur. J. Biochem. 177, 35-45, 1988
A;Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te
A;Reference number: S01790; MUID:89030693; PMID:3181157
A;Accession: S01790
A;Molecule type: mRNA
A;Residues: 2538-3084 <DEU>
A;Cross-references: EMBL:X13459; NID:g55499; PIDN:CAA31807.1; PID:g818014
A;Accession: A30451
A;Molecule type: protein
A;Residues: 1911-1929;1997-2006;2033-2045,'X',2047-2054,'X',2056-2066,'X',2068-2105;2120
470;2487-2498;2502-2525;2538-2557;2561-2591,'X',2593-2594;2600-2610;2616-2645;2648-2655;
93;2998-3005,'A',3007-3033,'V',3035;3068-3083 <DE2>
A;Note: 2256-Val was also found
R;Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
Lab. Invest. 60, 772-782, 1989
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A;Reference number: A34961; MUID:89280632; PMID:2733383
A;Accession: S14670
A;Molecule type: protein
A;Residues: 2424-2436;2440-2451;2461-2467;2487-2525;2550-2557;2561-2593;2600-2610;2616-2
-2942,'T',2944-2964;2969-2976;2980-2993;2998-3000,'I',3002-3018,'V',3020-3034;3068-3083
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-3084/Product: laminin alpha-1 chain #status predicted <MAT>
F;25-277/Domain: VI <DOM6>
F;277-331/Domain: laminin-type EGF-like homology <LE01>
F;278-519/Domain: V <DOM5>
F;334-401/Domain: laminin-type EGF-like homology <LE02>
F;404-458/Domain: laminin-type EGF-like homology <LE03>
F;461-507/Domain: laminin-type EGF-like homology <LE04>
F;510-519/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;520-715/Domain: IVb <DO4B>
F;716-1166/Domain: IIIb <DO3B>
```

```
F;716-746/Domain: laminin-type EGF-like homology #status atypical <LE06>
F;749-795/Domain: laminin-type EGF-like homology <LE07>
F;798-853/Domain: laminin-type EGF-like homology <LE08>
F;830-834/Region: cell adhesion #status predicted
F;856-906/Domain: laminin-type EGF-like homology <LE09>
F;909-955/Domain: laminin-type EGF-like homology <LE10>
F;958-1002/Domain: laminin-type EGF-like homology <LE11>
F;1005-1048/Domain: laminin-type EGF-like homology <LE12>
F;1051-1094/Domain: laminin-type EGF-like homology <LE13>
F;1097-1116/Domain: laminin-type EGF-like homology #status atypical <LE14>
F;1118-1154/Domain: laminin-type EGF-like homology #status atypical <LE15>
F;1147-1149/Region: cell attachment (R-G-D) motif
F;1157-1166/Domain: laminin-type EGF-like homology #status atypical <LE16>
F;1167-1368/Domain: IVa <DO4A>
F;1369-1561/Domain: IIIa <DO3A>
F;1369-1407/Domain: laminin-type EGF-like homology #status atypical <LE17>
F;1410-1456/Domain: laminin-type EGF-like homology <LE18>
F;1459-1513/Domain: laminin-type EGF-like homology <LE19>
F;1516-1560/Domain: laminin-type EGF-like homology <LE20>
F;1562-2133/Domain: II/I <DOM2>
F;1562-2133/Region: heptad repeats
F;2134-3084/Domain: G <DOMG>
F;2150-2308/Domain: laminin G repeat homology <LG1>
F;2337-2492/Domain: laminin G repeat homology <LG2>
F;2518-2683/Domain: laminin G repeat homology <LG3>
F;2748-2897/Domain: laminin G repeat homology <LG4>
F;2925-3082/Domain: laminin G repeat homology <LG5>
F;25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;45,79,370,374,531,562,672,808,914,959,969,1052,1344,1414,1586,1603,1659,1686,1706,1718
e (Asn) (covalent) #status predicted
F;304-312/Disulfide bonds: #status experimental
F;770,857,1999,2055,2067,2835/Binding site: carbohydrate (Asn) (covalent) #status experi
F;845,2102/Binding site: carbohydrate (Asn) (covalent) #status absent

  Query Match             9.5%;  Score 280;  DB 1;  Length 3084;
  Best Local Similarity   19.4%;  Pred. No. 6.5e-11;
  Matches  127;  Conservative  110;  Mismatches  222;  Indels  196;  Gaps   25;

Qy          7 SGVEVRLPNDLEDLKGY---TS--------LSLFLQRPDLRENGGTEDMFVMYLGNKDAS 55
              : ::| :  | : :: |   ||        |::  | |          |  : |||:  :|
Db       2122 ASIKVAVSADRDCIRAYQPQTSSTNYNTLILNVKTQEP---------DNLLFYLGS-SSS 2171

Qy         56 KDYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLN--Y 113
               |:: : :  |::  :::||      ::  :|   :   ::          | :|  :
Db       2172 SDFLAVEMRRGKVAFLWDLGSGSTRLEFPEVSINNNRWHSIY-------ITRFGNMGSLS 2224

Qy        114 TKEA---------TSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLR 164
              |||          ||  |    | |:   :::||:         :|||     :   ::
Db       2225 VKEASAAENPPVRTSKSPGPSKVLDI---NNSTLM---------FVGGLGGQIKKSPAVK 2272

Qy        165 FPPYKGCIELDDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNY-FEGTGYARIPT 223
             :|||:    ||   : |:|:         :   |    :  | :: |:|:||| :
Db       2273 VTHFKGCMGEAFLNGKSIGLWNYIE----REGKCNGCFGSSQNEDSSFHFDGSGYAMVEK 2328

Qy        224 QPNAPFPNFIQTIQTTVDRGLLFF--AENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIR 281
                  :   |    ||||:  :    :|:|: :  | : |   | | |
Db       2329 TLRPTVTQIVILFSTFSPNGLLFYLASNGTKDFLSIELVRGRVKVMVDLGSGP------- 2381

Qy        282 DTINDGKDHSILITIGKLQKRMWINVNERSVRIEGEIFDFSTY----------------- 324
                       |:|  :      |  :  :  | :| :  |  |
Db       2382 ---------LTLMTDRRYNNGTWYKIAFQRNRKQGLLAVFDAYDTSDKETKQGETPGAAS 2432

Qy        325 ----------YLGGIPIAIRERFNISTPAFQGCMKNLK-KTSGVVRLNDTVGVTKKCSED 373
                       |:||:| :   |  :|: :: ||:|||:   |    | :: || | |:
Db       2433 DLNRLEKDLIYVGGLPHSKAVRKGVSSRSYVGCIKNLEISRSTFDLLRNSYGVRKGCA-- 2490

Qy        374 WKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLL-NHQTRTSS--LLVTL 430
              : ::: || |||      :::|          ::  |  :||    |: ||  ||| |
Db       2491 LEPIQSVSFLRGGY-----VEMPP----------KSLSPESSLLATFATKNSSGILLVAL 2535

Qy        431 EDGHIELSTRDSNIPIFK-------------------------SPGTYMDGLLHHVSV 463
                    :::| |                             |:| ||  | :|:
Db       2536 GKDAEEAGGAQAHVPFFSIMLLEGRIEVHVNSGDGTSLRKALLHAPTGSYSDGQEHSISL 2595

Qy        464 ISDTSGLRLLIDDQVLRRNQRLPSFSNAQQSLRLG--------------GG-------- 500
              : :   : : :|:                |:   ::||              ||
Db       2596 VRNRRVITIQVDE-------------NSPVEMKLGPLTEGKTIDISNLYIGGLPEDKATP 2642

Qy        501 ------HFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPPLMLFK 549
                   | ||| ||::       ::||    :  :   |  | | : |   | :
Db       2643 MLKMRTSFHGCIKNVVL-----DAQLLDFTHATGSEQVELDTCLLAEEPMQSLHR 2692


RESULT 10
S14458
laminin alpha-1 chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S14458; S14663; A34961
R;Haaparanta, T.; Uitto, J.; Ruoslahti, E.; Engvall, E.
Matrix 11, 151-160, 1991
A;Title: Molecular cloning of the cDNA encoding human laminin A chain.
A;Reference number: S14458; MUID:91333420; PMID:1714537
A;Accession: S14458
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-3075 <HAA>
A;Cross-references: UNIPROT:P25391
R;Nissinen, M.; Vuolteenaho, R.; Boot-Handford, R.; Kallunki, P.; Tryggvason, K.
Biochem. J. 276, 369-379, 1991
A;Title: Primary structure of the human laminin A chain. Limited expression in human ti
A;Reference number: S14663; MUID:91264789; PMID:2049067
A;Accession: S14663
A;Molecule type: mRNA
A;Residues: 1-227,'FE',230-251,'MLP',255-418,'E',420-518,'L',520-1022,'V',1024-1074,'V'
A;Cross-references: EMBL:X58531; NID:g34225; PIDN:CAA41418.1; PID:g34226
R;Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
Lab. Invest. 60, 772-782, 1989
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 ch
A;Reference number: A34961; MUID:89280632; PMID:2733383
A;Accession: A34961
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 'W',2397-2745,'L',2747-3053,'L',3055-3072,'PSP' <OLS>
A;Note: the authors translated the codon AGA for residue 2692 as Pro
C;Genetics:
A;Gene: GDB:LAMA1; LAMA
A;Cross-references: GDB:120135; OMIM:150320
A;Map position: 18p11.32-18p11.22
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; disulfide bo
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-3075/Product: laminin alpha-1 chain #status predicted <MAT>
F;18-269/Domain: VI <DOM6>
F;270-516/Domain: V <DOM5>
F;270-324/Domain: laminin-type EGF-like homology <LE1>
F;327-394/Domain: laminin-type EGF-like homology <LE2>
F;397-451/Domain: laminin-type EGF-like homology <LE3>
F;454-500/Domain: laminin-type EGF-like homology <LE4>
F;503-512/Domain: laminin-type EGF-like homology #status atypical <LE5>
F;517-708/Domain: IVb <DO4B>
F;709-1159/Domain: IIIb <DO3B>
F;709-739/Domain: laminin-type EGF-like homology #status atypical <LE6>
F;742-788/Domain: laminin-type EGF-like homology <LE7>
F;791-846/Domain: laminin-type EGF-like homology <LE8>
F;849-899/Domain: laminin-type EGF-like homology <LE9>
F;902-948/Domain: laminin-type EGF-like homology <LE10>
F;951-995/Domain: laminin-type EGF-like homology <LE11>
F;998-1041/Domain: laminin-type EGF-like homology <LE12>
F;1044-1087/Domain: laminin-type EGF-like homology <LE13>
F;1090-1109/Domain: laminin-type EGF-like homology #status atypical <LE14>
F;1111-1147/Domain: laminin-type EGF-like homology #status atypical <LE15>
F;1150-1159/Domain: laminin-type EGF-like homology #status atypical <LE16>
F;1160-1361/Domain: IVa <DO4A>
F;1362-1553/Domain: IIIa <DO3A>
F;1362-1400/Domain: laminin-type EGF-like homology #status atypical <LE17>
```

```
F;1403-1449/Domain: laminin-type EGF-like homology <LE18>
F;1452-1506/Domain: laminin-type EGF-like homology <LE19>
F;1509-1553/Domain: laminin-type EGF-like homology <LE20>
F;1554-2125/Domain: I/II, heptad repeats <DOM2>
F;2116-2120/Region: cell adhesion #status predicted
F;2126-3075/Domain: G <DOMG>
F;2142-2300/Domain: laminin G repeat homology <LG1>
F;2329-2484/Domain: laminin G repeat homology <LG2>
F;2510-2676/Domain: laminin G repeat homology <LG3>
F;2534-2536/Region: cell attachment (R-G-D) motif
F;2739-2888/Domain: laminin G repeat homology <LG4>
F;2916-3073/Domain: laminin G repeat homology <LG5>
F;38,164,555,665,763,801,838,926,952,1045,1407,1579,1596,1678,1689,1698,1717,1804,1894,1
rate (Asn) (covalent) #status predicted
F;297-305/Disulfide bonds: #status predicted

  Query Match             9.2%;  Score 270;  DB 2;  Length 3075;
  Best Local Similarity   20.8%;  Pred. No. 3.3e-10;
  Matches  130;  Conservative  116;  Mismatches  262;  Indels  116;  Gaps   26;

Qy          7 SGVEVRLPNDLEDLKGY-----------TSLSLFLQRPDLRENGGTEDMFVMYLGNKDAS 55
              : ::| :  | : :: |             :|::  | |         |  : |||:  ||
Db       2114 ASIKVAVSADRDCIRAYQPQISSTNYNTLTLNVKTQEP---------DNLLFYLGSSTAS 2164

Qy         56 KDYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLN--Y 113
               |:: : :  |::  :::||     ::      :       ::        : :|  :
Db       2165 -DFLAVEMRRGRVAFLWDLGSGSTRLEFPDFPIDDNRWHSI-------HVARFGNIGSLS 2216

Qy        114 TKEATSNKPKAPAVYDLEGGSSNTL-LNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCI 172
               || :||: |:|       |::| | :|      : :|||     :    ::   :|||:
Db       2217 VKEMSSNQ-KSPTKTSKSPGTANVLDVN---NSTLMFVGGLGGQIKKSPAVKVTHFKGCL 2272

Qy        173 ELDDLNENVLSLYNFKTTFNLNTTEVE-PCR----RRKEESDKNYFEGTGYARIPTQPNA 227
                ||   : |:|:         | |  ||      : |    :|:|:||: :      |
Db       2273 GEAFLNGKSIGLWNY--------IEREGKCRGCFGSSQNEDPSFHFDGSGYSVVEKSLPA 2324

Qy        228 PFPNFIQTIQTTVDRGLLFF--AENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTIN 285
                |    |    ||| :  :   :|:|: :  | : |   | | |       |   |
Db       2325 TVTQIIMLFNTFSPNGLLLYLGSYGTKDFLSIELFRGRVKVMTDLGSGPITLLTDR-RYN 2383

Qy        286 DGKDHSILITIGKLQKRMWI----NVNERSVRIEGEI---------FDFSTYYLGGIPIA 332
              :|  : |      : |  : :    | : :  : :||           |     |:||:| :
Db       2384 NGTWYKIAFQRNRKQGVLAVIDAYNTSNKETK-QGETPGASSDLNRLDKDPIYVGGLPRS 2442

Qy        333 IRERFNISTPAFQGCMKNLK-KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFT 391
                |  ::| :| ||:|||:    |     | :: || | |    : :|: || :|| :
Db       2443 RVVRRGVTTKSFVGCIKNLEISRSTFDLLRNSYGVRKGCL--LEPIRSVSFLKGGYIELP 2500

Qy        392 NLDVPSTDRFQLSFGFQTFQPSGTLL-----------NHQTRTSSLLVTLEDGHIELST 439
              :     : ::|   | || :|             :       | |  |:||:
Db       2501 PKSLSPESEWLVTFA--TTNSSGIILAALGGDVEKRGDREEAHVPFFSVMLIGGNIEVHV 2558

Qy        440 RDSN-----IPIFKSP-GTYMDGLLHHVSVISDTSGLRLLIDDQ---VLRRNQRLPSFSN 490
                :       :  :| ||  ||  | :|:: :   : : :|:     ::    : | :
Db       2559 NPGDGTGLRKALLHAPTGTCSDGQAHSISLVRNRRIITVQLDENNPVEMKLGTLVESRTI 2618

Qy        491 AQQSLRLGG-------------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGC 537
                :| :||               | ||| |::      : |:||  |    :   |  |
Db       2619 NVSNLYVGGIPEGEGTSLLTMRRSFHGCIKNLIF-----NLELLDFNSAVGHEQVDLDTC 2673

Qy        538 SLNKPPPFL-------MLFKSPKRF 554
               |:: | |       | : |: |
Db       2674 WLSERPKLAPDAEDSKLLREPRAF 2697


RESULT 11
T43291
laminin alpha chain - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43291
R;Zhu, X.; Kao, G.; Joh, K.; Hall, D.H.; Wadsworth, V.K.; Hutter, H.; Vogel, B.E.; Huang
submitted to the EMBL Data Library, June 1998
A;Description: Expression, function and evolution of laminin alpha chains.
A;Reference number: Z22397
A;Accession: T43291
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3102 <ZHU>
A;Cross-references: UNIPROT:O45614; EMBL:AF074902; PIDN:AAC26793.1
C;Genetics:
A;Map position: 1
A;Note: lama1/2
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

  Query Match             8.4%;  Score 247;  DB 2;  Length 3102;
  Best Local Similarity   22.1%;  Pred. No. 1.5e-08;
  Matches  128;  Conservative  108;  Mismatches  210;  Indels  134;  Gaps   30;

Qy         50 GNKDASKDYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAV--MDRVKFQRIYQ 107
                | :    ::: : : | ::   :::|  :       :::| |      |   ||| :  |
Db       2308 GRRTQPSEHLAVEIRDKRVVVHWDIGSGK------KMITNSHPINYVPSNDRVTWYHIDV 2361

Qy        108 FA---KLNYT---KEATSN--KPKAPAVYDLEGGS--SNTLLNLDPEDAVFYVGGYPPDF 157
                     :| |   ||:     ||:    |     | |   |:: |  | :    ||    |
Db       2362 LRIGNAVNLTVALKESYDGGFKPRGAPVSVFVGNSKDDNSIFNTIPGETTIDVG---TDE 2418

Qy        158 ELPSRLRFPPYK-----GCIELDDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNY 212
               : | :    :|     | : :|::    | |::|::|    | | |       : | : :
Db       2419 TVASDIGLTTHKFSGIVGGLRIDEV---PLPLWSFEST----TGECEGATSPPKTSQRGH 2471

Qy        213 FEGTGYARIPTQPNAPFPNFIQTIQTTVD-RGLLFF--AENQDNFISLNIEDGNLMVRYK 269
                |:| :    :    : |  |        |||:|  :|   :|::: : || :| :
Db       2472 LFRDGFANVSMSVSERTMSAITVIFNAFSPNGLLYFRGSEASGDFVAIYLNDGKVMFKIN 2531

Qy        270 LNSEPPKEKGIRDTINDGKDHSI-LITIGKLQKRMWINVNERSVR----IEGE----IFD 320
               |       |   ::  ||||:|::  |  |      |:: |:  : |    | ||      :
Db       2532 LGGGSVAELTSQNVYNDGKEHTVKAIRTG---SEMYLQVDSDADRFNTVITGENTALNIE 2588

Qy        321 FSTYYLGGIPIAI-RERF-NISTPAFQGCMKNLK----------------KTSGVVRLN 361
                :|: |:|: : :| | :|:    | ||:  :|                || |  :::
Db       2589 NENHYVAGVPMTLNKEVFGDINWNGFIGCILTVKPSQVGELDLDHPEHSQGKTDGCSQVS 2648

Qy        362 DTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQT 421
               |||  |             | : | :    : : ::  |  :| |:|  : :|||:   :
Db       2649 ---GVTDK---------IIGFPKPGYLITKGISIDNSSTF--AFSFRTREENGTLVYQSS 2694

Qy        422 RTSSLLVTLED------GHI--------------ELSTRDSNIPIFKSPGTYMDGLLHH 460
               :     |:  |      |:|              : |:|   :  |:|   | || :|
Db       2695 KLQK--VSKRDSEDDGKGYIAFYLFRGYLVLHFGKDASSR-KEVVTFRSSHPYNDGQVHA 2751

Qy        461 VSVISDTSGLRLLIDDQVLRRNQRL---PSFSNAQQSLRLGG--------------GHF 502
               | :  :   : : :||: :  :| |     |  |||                   |
Db       2752 VFMERNGKIISVKVDDKEIGDSQSLSDETSVGTTSGRLILGGFSDDLKPPNNEIPITSFF 2811

Qy        503 EGCISNVL--VQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ||||:|   ::| | :||          | :| :| ||::
Db       2812 IGCISDVFLNMKRVSLAPE---------KHNAQIGMCSMD 2842


RESULT 12
F87908
protein T22A3.8 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F87908; E87908
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: F87908
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2823 <STO>
```

A;Cross-references: UNIPROT:O45614; GB:chr_I; PIDN:CAA15432.1; PID:g3924779; GSPDB:GN000
A;Accession: E87908
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2823 <ST2>
A;Cross-references: GB:chr_I; PIDN:CAB03385.1; PID:g3924881; GSPDB:GN00019; CESP:T22A3.8
C;Genetics:
A;Gene: T22A3.8
A;Map position: 1
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match 7.6%; Score 222.5; DB 2; Length 2823;
Best Local Similarity 21.7%; Pred. No. 7e-07;
Matches 119; Conservative 102; Mismatches 205; Indels 123; Gaps 28;

```
Qy        50 GNKDASKDYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAV--MDRVKFQRIYQ 107
             | :    ::: : :. | ::   :::|  :      :::| |      |   ||| :  |
Db      2308 GRRTQPSEHLAVEIRDKRVVVHWDIGSGK------KMITNSHPINYVPSNDRVTWYHIDV 2361

Qy       108 FA---KLNYT---KEATSN--KPKAPAVYDLEGGS--SNTLLNLDPEDAVFYVGGYPPDF 157
               :| |   ||:      ||:    |    | |   |:: |  | :    ||    |
Db      2362 LRIGNAVNLTVALKESYDGGFKPRGAPVSVFVGNSKDDNSIFNTIPGETTIDVG---TDE 2418

Qy       158 ELPSRLRFPPYK-----GCIELDDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNY 212
              : | :    :|     | : :|::    | |::|::|    | | |      : | : :
Db      2419 TVASDIGLTTHKFSGIVGGLRIDEV---PLPLWSFEST----TGECEGATSPPKTSQRGH 2471

Qy       213 FEGTGYARIPTQPNAPFPNFIQTIQTTVD-RGLLFF--AENQDNFISLNIEDGNLMVRYK 269
                |:| :    :   : | |      |||:|  :|   :|::: : || :| :
Db      2472 LFRDGFANVSMSVSERTMSAITVIFNAFSPNGLLYFRGSEASGDFVAIYLNDGKVMFKIN 2531

Qy       270 LNSEPPKEKGIRDTINDGKDHSI-LITIGKLQKRMWINVNERSVR----IEGE----IFD 320
             |      |   ::  ||||:|::  | |      |:: |:  : |    | ||      :
Db      2532 LGGGSVAELTSQNVYNDGKEHTVKAIRTG---SEMYLQVDSDADRFNTVITGENTALNIE 2588

Qy       321 FSTYYLGGIPIAI-RERF-NISTPAFQGCMKNLK----------------KTSGVVRLN 361
                :|: |:|: : :| | :|:   | ||:  :|                 || |  :::
Db      2589 NENHYVAGVPMTLNKEVFGDINWNGFIGCILTVKPSQVGELDLDHPEHSQGKTDGCSQVS 2648

Qy       362 DTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQT 421
               ||| |          | : | :    : : ::  |  :| |:| : :|||:    :
Db      2649 ---GVTDK---------IIGFPKPGYLITKGISIDNSSTF--AFSFRTREENGTLVYQSS 2694

Qy       422 RTSSLLVTLED------GHI--------------ELSTRDSNIPIFKSPGTYMDGLLHH 460
             :     |:  |      |:|              : |:|   :  |:|   | || :|
Db      2695 KLQK--VSKRDSEDDGKGYIAFYLFRGYLVLHFGKDASSR-KEVVTFRSSHPYNDGQVHA 2751

Qy       461 VSVISDTSGLRLLIDDQVLRRNQRL---PSFSNAQQSLRLGG--------------GHF 502
             | :  :   : : :||: :  :| |     |       | |||              |
Db      2752 VFMERNGKIISVKVDDKEIGDSQSLSDETSVGTTSGRLILGGFSDDLKPPNNEIPITSFF 2811

Qy       503 EGCISNVLV 511
              ||||:| :
Db      2812 IGCISDVFL 2820
```

RESULT 13
T23064
hypothetical protein T22A3.8 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23064; T25096
R;Barlow, K.
submitted to the EMBL Data Library, October 1997
A;Reference number: Z19669
A;Accession: T23064
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2823 <WIL>
A;Cross-references: UNIPROT:O45614; EMBL:AL008585; PIDN:CAA15432.1; GSPDB:GN00019; CESP:
A;Experimental source: clone H10E24
R;McMurray, A.
submitted to the EMBL Data Library, October 1996

A;Reference number: Z19980
A;Accession: T25096
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2823 <WI2>
A;Cross-references: EMBL:Z81125; PIDN:CAB03385.1; GSPDB:GN00019; CESP:T22A3.8
A;Experimental source: clone T22A3
C;Genetics:
A;Gene: CESP:T22A3.8
A;Map position: 1
A;Introns: 45/1; 282/2; 312/3; 416/2; 1255/3; 1329/3; 1418/3; 1776/2; 1988/2; 2760/2
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like

Query Match 7.6%; Score 222.5; DB 2; Length 2823;
Best Local Similarity 21.7%; Pred. No. 7e-07;
Matches 119; Conservative 102; Mismatches 205; Indels 123; Gaps 28;

```
Qy        50 GNKDASKDYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAV--MDRVKFQRIYQ 107
             | :    ::: : :. | ::   :::|  :      :::| |      |   ||| :  |
Db      2308 GRRTQPSEHLAVEIRDKRVVVHWDIGSGK------KMITNSHPINYVPSNDRVTWYHIDV 2361

Qy       108 FA---KLNYT---KEATSN--KPKAPAVYDLEGGS--SNTLLNLDPEDAVFYVGGYPPDF 157
               :| |   ||:      ||:    |    | |   |:: |  | :    ||    |
Db      2362 LRIGNAVNLTVALKESYDGGFKPRGAPVSVFVGNSKDDNSIFNTIPGETTIDVG---TDE 2418

Qy       158 ELPSRLRFPPYK-----GCIELDDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNY 212
              : | :    :|     | : :|::    | |::|::|    | | |      : | : :
Db      2419 TVASDIGLTTHKFSGIVGGLRIDEV---PLPLWSFEST----TGECEGATSPPKTSQRGH 2471

Qy       213 FEGTGYARIPTQPNAPFPNFIQTIQTTVD-RGLLFF--AENQDNFISLNIEDGNLMVRYK 269
                |:| :    :   : | |      |||:|  :|   :|::: : || :| :
Db      2472 LFRDGFANVSMSVSERTMSAITVIFNAFSPNGLLYFRGSEASGDFVAIYLNDGKVMFKIN 2531

Qy       270 LNSEPPKEKGIRDTINDGKDHSI-LITIGKLQKRMWINVNERSVR----IEGE----IFD 320
             |      |   ::  ||||:|::  | |      |:: |:  : |    | ||      :
Db      2532 LGGGSVAELTSQNVYNDGKEHTVKAIRTG---SEMYLQVDSDADRFNTVITGENTALNIE 2588

Qy       321 FSTYYLGGIPIAI-RERF-NISTPAFQGCMKNLK----------------KTSGVVRLN 361
                :|: |:|: : :| | :|:   | ||:  :|                 || |  :::
Db      2589 NENHYVAGVPMTLNKEVFGDINWNGFIGCILTVKPSQVGELDLDHPEHSQGKTDGCSQVS 2648

Qy       362 DTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQT 421
               ||| |          | : | :    : : ::  |  :| |:| : :|||:    :
Db      2649 ---GVTDK---------IIGFPKPGYLITKGISIDNSSTF--AFSFRTREENGTLVYQSS 2694

Qy       422 RTSSLLVTLED------GHI--------------ELSTRDSNIPIFKSPGTYMDGLLHH 460
             :     |:  |      |:|              : |:|   :  |:|   | || :|
Db      2695 KLQK--VSKRDSEDDGKGYIAFYLFRGYLVLHFGKDASSR-KEVVTFRSSHPYNDGQVHA 2751

Qy       461 VSVISDTSGLRLLIDDQVLRRNQRL---PSFSNAQQSLRLGG--------------GHF 502
             | :  :   : : :||: :  :| |     |       | |||              |
Db      2752 VFMERNGKIISVKVDDKEIGDSQSLSDETSVGTTSGRLILGGFSDDLKPPNNEIPITSFF 2811

Qy       503 EGCISNVLV 511
              ||||:| :
Db      2812 IGCISDVFL 2820
```

RESULT 14
A48216
neurexin III-alpha secreted type 1 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Dec-2002
C;Accession: A48216; B48216
R;Ushkaryov, Y.A.; Suedhof, T.C.
Proc. Natl. Acad. Sci. U.S.A. 90, 6410-6414, 1993
A;Title: Neurexin IIIalpha: extensive alternative splicing generates membrane-bound and
A;Reference number: A48216; MUID:93342001; PMID:8341647
A;Accession: A48216
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1438 <USH>
A;Cross-references: GB:L14851

```
A;Accession: B48216
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1368,1372-1438 <US2>
A;Cross-references: GB:L14851
C;Genetics:
A;Introns: 1372/1
C;Superfamily: neurexin; EGF homology
C;Keywords: alternative splicing; brain; cell surface component; duplication; extracellu
F;1-27/Domain: signal sequence #status predicted <SIG>
F;202-234/Domain: EGF homology <EGF>
F;651-683/Domain: EGF homology <EGF1>

  Query Match             7.2%;  Score 212.5;  DB 2;  Length 1438;
  Best Local Similarity   20.6%;  Pred. No. 1.3e-06;
  Matches  118;  Conservative   72;  Mismatches  185;  Indels  199;  Gaps   26;

Qy         36 RENGGTEDMFVMYLGNKDASKDYIGMAVVDGQLTCVYNLGD------------------ 76
              : ||       ::: |    | ||: :|: || :: | |||
Db        295 QRNG-----LILHTGK---SADYVNLALKDGAVSLVINLGSGAFEAIVEPVNGKFNDNAW 346

Qy         77 ---------REAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSNKPKAPAV 127
                      |:  : :| :|| :                          ||:|
Db        347 HDVKVTRNLRQVTISVDGILTTT--------------------GYTQE----------- 374

Qy        128 YDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIE------------- 173
                    |:|      |  ||||| |   :||       : ||::
Db        375 -------DYTMLG---SDDFFYVGGSPSTADLPGSPVSNNFMGCLKEVVYKNNDIRLELS 424

Qy        174 -LDDLNENVLSLYN---FKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPF 229
               |  : :  : :|    ||      |   ::|           |:      |  :|
Db        425 RLARIGDTKMKIYGEVVFKCE---NVATLDPI---------NFETPEAYISLPKWNTKRM 472

Qy        230 PNFIQTIQTTVDRGLLFFA-----ENQD---------NFISLNIEDGNLMVRYKLNSEPP 275
               :   :||   ||: |      | :|          :| :: : |||| :   : |
Db        473 GSISFDFRTTEPNGLILFTHGKPQERKDVRSQKNTKVDFFAVELLDGNLYLLLDMGSGTI 532

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNERSVRI----EGEIFDF-STYYLGGIP 330
               |  :   |||: :   : | :  :   |:|| |        | || |     ||||:|
Db        533 KVKATQKKANDGEWYH--VDIQRDGRSGTISVNSRRTPFTASGESEILDLEGDMYLGGLP 590

Qy        331 IAIRERFNISTP----------AFQGCMKNL------KKTSGVVRLNDTVGVTKKCS--- 371
                  |  : |           : ||:::|      |    :  : :  ||   ||
Db        591 ---ENRAGLILPTELWTAMLNYGYVGCIRDLFIDGRSKNIRQLAEMQNAAGVKSSCSRMS 647

Qy        372 ----------------EDWK--------------LVRTAS-FSRGGQMSFTNLDVP--- 396
                           : |                | ||  |  | | :  : :|
Db        648 AKQCDSYPCKNNAVCKDGWNRFICDCTGTGYWGRTCEREASILSYDGSM-YMKVIMPMVM 706

Qy        397 STDRFQLSFGFQTFQPSGTLLNHQTRTS--SLLVTLEDGHIELSTRDSNIPI----FKSP 450
               |:   :|| | : :  | |:   :| |  :| : |: | ::|       | |      | |
Db        707 HTEAEDVSFRFMSQRAYGLLVATTSRDSADTLRLELDGGRVKLMVNLDCIRINCNSSKGP 766

Qy        451 GTYM------DGLLHHVSVISDTSGLRLLIDDQV 478
               |       |   | | |:     |:| :|| |
Db        767 ETLYAGQKLNDNEWHTVRVVRRGKSLKLTVDDDV 800


RESULT 15
B48218
neurexin III-alpha membrane-bound type 3 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Dec-2002
C;Accession: B48218; C48218
R;Ushkaryov, Y.A.; Suedhof, T.C.
Proc. Natl. Acad. Sci. U.S.A. 90, 6410-6414, 1993
A;Title: Neurexin IIIalpha: extensive alternative splicing generates membrane-bound and
A;Reference number: A48216; MUID:93342001; PMID:8341647
A;Accession: B48218
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1471 <USH>
A;Cross-references: GB:L14851
```

```
A;Accession: C48218
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1368,1372-1471 <US2>
A;Cross-references: GB:L14851
C;Genetics:
A;Introns: 1372/1
C;Superfamily: neurexin; EGF homology
C;Keywords: alternative splicing; brain; cell surface component; duplication; receptor;
F;1-27/Domain: signal sequence #status predicted <SIG>
F;202-234/Domain: EGF homology <EGF>
F;651-683/Domain: EGF homology <EGF1>

  Query Match             7.2%;  Score 212.5;  DB 2;  Length 1471;
  Best Local Similarity   20.6%;  Pred. No. 1.3e-06;
  Matches  118;  Conservative   72;  Mismatches  185;  Indels  199;  Gaps   26;

Qy         36 RENGGTEDMFVMYLGNKDASKDYIGMAVVDGQLTCVYNLGD------------------ 76
              : ||       ::: |    | ||: :|: || :: | |||
Db        295 QRNG-----LILHTGK---SADYVNLALKDGAVSLVINLGSGAFEAIVEPVNGKFNDNAW 346

Qy         77 ---------REAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSNKPKAPAV 127
                      |:  : :| :|| :                          ||:|
Db        347 HDVKVTRNLRQVTISVDGILTTT--------------------GYTQE----------- 374

Qy        128 YDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIE------------- 173
                    |:|      |  ||||| |   :||       : ||::
Db        375 -------DYTMLG---SDDFFYVGGSPSTADLPGSPVSNNFMGCLKEVVYKNNDIRLELS 424

Qy        174 -LDDLNENVLSLYN---FKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPF 229
               |  : :  : :|    ||      |   ::|           |:      |  :|
Db        425 RLARIGDTKMKIYGEVVFKCE---NVATLDPI---------NFETPEAYISLPKWNTKRM 472

Qy        230 PNFIQTIQTTVDRGLLFFA-----ENQD---------NFISLNIEDGNLMVRYKLNSEPP 275
               :   :||   ||: |      | :|          :| :: : |||| :   : |
Db        473 GSISFDFRTTEPNGLILFTHGKPQERKDVRSQKNTKVDFFAVELLDGNLYLLLDMGSGTI 532

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNERSVRI----EGEIFDF-STYYLGGIP 330
               |  :   |||: :   : | :  :   |:|| |        | || |     ||||:|
Db        533 KVKATQKKANDGEWYH--VDIQRDGRSGTISVNSRRTPFTASGESEILDLEGDMYLGGLP 590

Qy        331 IAIRERFNISTP----------AFQGCMKNL------KKTSGVVRLNDTVGVTKKCS--- 371
                  |  : |           : ||:::|      |    :  : :  ||   ||
Db        591 ---ENRAGLILPTELWTAMLNYGYVGCIRDLFIDGRSKNIRQLAEMQNAAGVKSSCSRMS 647

Qy        372 ----------------EDWK--------------LVRTAS-FSRGGQMSFTNLDVP--- 396
                           : |                | ||  |  | | :  : :|
Db        648 AKQCDSYPCKNNAVCKDGWNRFICDCTGTGYWGRTCEREASILSYDGSM-YMKVIMPMVM 706

Qy        397 STDRFQLSFGFQTFQPSGTLLNHQTRTS--SLLVTLEDGHIELSTRDSNIPI----FKSP 450
               |:   :|| | : :  | |:   :| |  :| : |: | ::|       | |      | |
Db        707 HTEAEDVSFRFMSQRAYGLLVATTSRDSADTLRLELDGGRVKLMVNLDCIRINCNSSKGP 766

Qy        451 GTYM------DGLLHHVSVISDTSGLRLLIDDQV 478
               |       |   | | |:     |:| :|| |
Db        767 ETLYAGQKLNDNEWHTVRVVRRGKSLKLTVDDDV 800


Search completed: February 22, 2005, 08:19:38
Job time : 18.0758 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:07:29 ; Search time 95.5943 Seconds
(without alignments)
3026.590 Million cell updates/sec

Title: US-10-817-423-4
Perfect score: 2940
Sequence: 1 MRFNGKSGVEVRLPNDLEDL.....MLFKSPKRFNKGRIFNVNQL 565

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2940	100.0	1725	2	P70570	P70570 rattus norv
2	2704	92.0	3333	1	LMA3_MOUSE	Q61789 mus musculu
3	2441	83.0	1668	2	Q6VU69	Q6vu69 homo sapien
4	2441	83.0	3277	2	Q6VU67	Q6vu67 homo sapien
5	2441	83.0	3333	2	Q6VU68	Q6vu68 homo sapien
6	2439	83.0	1713	1	LMA3_HUMAN	Q16787 homo sapien
7	2439	83.0	1806	2	Q96TG0	Q96tg0 homo sapien
8	2439	83.0	3333	2	Q76E14	Q76e14 homo sapien
9	2224.5	75.7	1725	2	Q867A1	Q867a1 canis famil
10	712	24.2	3695	1	LMA5_HUMAN	O15230 homo sapien
11	712	24.2	3695	2	Q8TDF8	Q8tdf8 homo sapien
12	686	23.3	1816	1	LMA4_HUMAN	Q16363 homo sapien
13	685	23.3	1254	2	Q91VV0	Q91vv0 mus musculu
14	685	23.3	1816	1	LMA4_MOUSE	P97927 mus musculu
15	683	23.2	1524	2	Q6ZQA1	Q6zqa1 mus musculu
16	681	23.2	3718	1	LMA5_MOUSE	Q61001 mus musculu
17	492.5	16.8	670	2	Q9BTT3	Q9btt3 homo sapien
18	395	13.4	3712	1	LMA_DROME	Q00174 drosophila
19	395	13.4	3712	2	Q9VRW0	Q9vrw0 drosophila
20	359	12.2	3616	2	Q7PPF9	Q7ppf9 anopheles g
21	326	11.1	794	2	Q8R3Y7	Q8r3y7 mus musculu
22	302	10.3	3106	1	LMA2_MOUSE	Q60675 mus musculu
23	298.5	10.2	1518	2	Q21442	Q21442 caenorhabdi
24	298.5	10.2	3672	1	LML2_CAEEL	Q21313 caenorhabdi
25	298.5	10.2	3704	2	P91904	P91904 caenorhabdi
26	294	10.0	3110	1	LMA2_HUMAN	P24043 homo sapien
27	285.5	9.7	858	2	Q8R145	Q8r145 mus musculu
28	280	9.5	3084	1	LMA1_MOUSE	P19137 mus musculu
29	270	9.2	3075	1	LMA1_HUMAN	P25391 homo sapien
30	247	8.4	3102	2	O45614	O45614 caenorhabdi
31	219.5	7.5	1247	2	Q7PT06	Q7pt06 anopheles g
32	216	7.3	1392	2	Q8IUE3	Q8iue3 homo sapien
33	213.5	7.3	1541	1	NX3A_HUMAN	Q9y4c0 homo sapien
34	213	7.2	3375	2	Q8IP51	Q8ip51 drosophila
35	212.5	7.2	1203	2	Q6ZQ56	Q6zq56 mus musculu
36	212.5	7.2	1587	2	Q6P9K9	Q6p9k9 mus musculu
37	207.5	7.1	1363	1	NX1A_CHICK	Q9ddd0 gallus gall
38	204.5	7.0	1514	1	NX1A_RAT	Q63372 rattus norv
39	200	6.8	1553	2	Q8CHE6	Q8che6 mus musculu
40	199.5	6.8	1530	1	NX1A_BOVIN	Q28146 bos taurus
41	198	6.7	1176	2	Q80Y87	Q80y87 mus musculu
42	197	6.7	1560	2	Q18291	Q18291 caenorhabdi
43	196	6.7	1477	1	NX1A_HUMAN	Q9ulb1 homo sapien
44	196	6.7	3367	2	Q9XZC9	Q9xzc9 drosophila
45	195.5	6.6	747	2	Q7Z5W6	Q7z5w6 homo sapien

ALIGNMENTS

RESULT 1
P70570
ID P70570 PRELIMINARY; PRT; 1725 AA.
AC P70570;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Laminin-5 alpha 3 chain.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97081969; PubMed=8923212;
RA Baker S.E., Hopkinson S.B., Fitchmun M., Andreason G.L., Frasier F.,
RA Plopper G., Quaranta V., Jones J.C.R.;
RT "Laminin-5 and hemidesmosomes: role of the alpha 3 chain subunit in
RT hemidesmosome stability and assembly.";
RL J. Cell Sci. 109:2509-2520(1996).
DR EMBL; U61261; AAB17053.1; -.
DR HSSP; P35070; 1IP0.
DR GO; GO:0005606; C:laminin-1; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR GO; GO:0030334; P:regulation of cell migration; IEA.
DR GO; GO:0045995; P:regulation of embryonic development; IEA.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00053; Laminin_EGF; 2.
DR Pfam; PF02210; Laminin_G_2; 4.
DR Pfam; PF06008; Laminin_I; 1.
DR Pfam; PF06009; Laminin_II; 1.
DR SMART; SM00180; EGF_Lam; 2.
DR SMART; SM00282; LamG; 5.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW Laminin EGF-like domain.
SQ SEQUENCE 1725 AA; 190392 MW; 02EE43B33E72B0FB CRC64;

Query Match 100.0%; Score 2940; DB 2; Length 1725;
Best Local Similarity 100.0%; Pred. No. 2.7e-191;
Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db        782 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 841

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 901

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 961

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 1021

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 1081

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 1141

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 1201

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 1261

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 1321

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              |||||||||||||||||||||||||
Db       1322 KPPFLMLFKSPKRFNKGRIFNVNQL 1346
```

RESULT 2
LMA3_MOUSE
ID   LMA3_MOUSE   STANDARD;   PRT; 3333 AA.
AC   Q61789; O08751; Q61788; Q61966; Q9JHQ7;
DT   01-NOV-1997 (Rel. 35, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Laminin alpha-3 chain precursor (Nicein alpha subunit).
GN   Name=Lama3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE OF 1-58 FROM N.A., AND SEQUENCE OF 32-38.
RX   MEDLINE=21818471; PubMed=11829758; DOI=10.1042/0264-6021:3620213;
RA   Garbe J.H., Gohring W., Mann K., Timpl R., Sasaki T.;
RT   "Complete sequence, recombinant analysis and binding to laminins and
RT   sulphated ligands of the N-terminal domains of laminin alpha3B and
RT   alpha5 chains.";
RL   Biochem. J. 362:213-221(2002).
RN   [2]
RP   SEQUENCE OF 1-726 FROM N.A.
RC   STRAIN=ICR;
RX   MEDLINE=97296337; PubMed=9151674; DOI=10.1083/jcb.137.3.685;
RA   Miner J.H., Patton B.L., Lentz S.I., Gilbert D.J., Snider W.D.,
RA   Jenkins N.A., Copeland N.G., Sanes J.R.;
RT   "The laminin alpha chains: expression, developmental transitions, and
RT   chromosomal locations of alpha1-5, identification of heterotrimeric
RT   laminins 8-11, and cloning of a novel alpha3 isoform.";
RL   J. Cell Biol. 137:685-701(1997).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM A), AND SEQUENCE OF 716-3284 FROM N.A.
RP   (ISOFORM B).
RC   STRAIN=BALB/c; TISSUE=Lung;
RX   MEDLINE=95394948; PubMed=7665604; DOI=10.1074/jbc.270.37.21820;
RA   Galliano M.-F., Aberdam D., Aguzzi A., Ortonne J.-P., Meneguzzi G.;
RT   "Cloning and complete primary structure of the mouse laminin alpha 3
RT   chain. Distinct expression pattern of the laminin alpha 3A and alpha
RT   3B chain isoforms.";
RL   J. Biol. Chem. 270:21820-21826(1995).
RN   [4]
RP   REVISIONS.
RA   Aberdam D.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 1767-2485 FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=94281750; PubMed=8012114;
RA   Aberdam D., Galliano M.-F., Mattei M.-G., Pisani-Spadafora A.,
RA   Ortonne J.-P., Meneguzzi G.;
RT   "Assignment of mouse nicein genes to chromosomes 1 and 18.";
RL   Mamm. Genome 5:229-233(1994).
RN   [6]
RP   SEQUENCE OF 1767-2485 FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=94363405; PubMed=8081888;
RA   Aberdam D., Aguzzi A., Baudoin C., Galliano M.-F., Ortonne J.-P.,
RA   Meneguzzi G.;
RT   "Developmental expression of nicein adhesion protein (laminin-5)
RT   subunits suggests multiple morphogenic roles.";
RL   Cell Adhes. Commun. 2:115-129(1994).
CC   -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC   is thought to mediate the attachment, migration and organization
CC   of cells into tissues during embryonic development by interacting
CC   with other extracellular matrix components.
CC   -!- FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
CC   via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-
CC   6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine
CC   phosphorylation of pp125-FAK and p80, (3) differentiation of
CC   keratinocytes (By similarity).
CC   -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC   different polypeptide chains (alpha, beta, gamma), which are bound
CC   to each other by disulfide bonds into a cross-shaped molecule
CC   comprising one long and three short arms with globules at each
CC   end. The alpha-3 chain is a subunit of laminin-5
CC   (epiligrin/kalinin/nicein), and possibly also a component of
CC   laminin-6 (K-laminin) and laminin-7 (KS-laminin).
CC   -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC   membranes (major component).
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=2;
CC   Name=B;
CC   IsoId=Q61789-1; Sequence=Displayed;
CC   Name=A;
CC   IsoId=Q61789-2; Sequence=VSP_003038, VSP_003039;
CC   -!- TISSUE SPECIFICITY: Basal membrane of the upper alimentary tract
CC   and urinary and nasal epithelia, salivary glands and teeth (both
CC   variants). Isoform A is predominantly expressed in skin, hair
CC   follicles and developing neurons of the trigeminal ganglion.
CC   Isoform B was found in bronchi, alveoli, stomach, intestinal
CC   crypts, whisker pads, CNS, telencephalic neuroectoderm, thalamus,
CC   Rathke's pouch and periventricular subependymal germinal layer.
CC   -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC   with other laminin chains to form a coiled coil structure.
CC   -!- DOMAIN: Domains IV and G are globular.
CC   -!- SIMILARITY: Contains 15 laminin EGF-like domains.
CC   -!- SIMILARITY: Contains 5 laminin G-like domains.
CC   -!- SIMILARITY: Contains 1 laminin IV domain.
CC   -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC   ---

```
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AJ293592; CAB99254.2; -.
DR   EMBL; U88353; AAC53179.1; -.
DR   EMBL; X84014; CAA58837.1; -.
DR   EMBL; X84013; CAA58836.1; ALT_FRAME.
DR   EMBL; L20478; AAA68091.1; -.
DR   HSSP; P02468; 1NPE.
DR   MGD; MGI:99909; Lama3.
DR   GO; GO:0005604; C:basement membrane; IDA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR008212; Lam_N2.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR008211; Laminin_N.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 10.
DR   Pfam; PF00054; Laminin_G; 3.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   Pfam; PF00055; Laminin_N; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   ProDom; PD003031; Laminin_B; 1.
DR   PROSITE; PS00022; EGF_1; 10.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 10.
KW   Alternative splicing; Basement membrane; Cell adhesion; Coiled coil;
KW   Direct protein sequencing; Extracellular matrix; Glycoprotein;
KW   Laminin EGF-like domain; Repeat; Signal.
FT   SIGNAL       1     31
FT   CHAIN       32   3333       Laminin alpha-3 chain.
FT   DOMAIN      32    294       Laminin N-terminal (domain VI).
FT   DOMAIN     295    725       Domain V.
FT   DOMAIN     296    350       Laminin EGF-like 1.
FT   DOMAIN     353    420       Laminin EGF-like 2.
FT   DOMAIN     423    464       Laminin EGF-like 3.
FT   DOMAIN     488    530       Laminin EGF-like 4.
FT   DOMAIN     533    576       Laminin EGF-like 5.
FT   DOMAIN     582    625       Laminin EGF-like 6.
FT   DOMAIN     628    678       Laminin EGF-like 7.
FT   DOMAIN     681    725       Laminin EGF-like 8.
FT   DOMAIN     793   1262       Laminin domain IV 1 (domain IV B).
FT   DOMAIN    1263   1464       Domain III B.
FT   DOMAIN    1310   1353       Laminin EGF-like 9.
FT   DOMAIN    1354   1403       Laminin EGF-like 10.
FT   DOMAIN    1404   1454       Laminin EGF-like 11.
FT   DOMAIN    1455   1464       Laminin EGF-like 12 (N-terminal).
FT   DOMAIN    1465   1653       Laminin domain IV (domain IV A).
FT   DOMAIN    1654   1821       Domain III A.
FT   DOMAIN    1654   1686       Laminin EGF-like 12 (C-terminal).
FT   DOMAIN    1687   1733       Laminin EGF-like 13.
FT   DOMAIN    1734   1786       Laminin EGF-like 14.
FT   DOMAIN    1787   1821       Laminin EGF-like 15 (incomplete).
FT   DOMAIN    1822   2388       Domain II and I.
FT   DOMAIN    2389   2590       Laminin G-like 1.
FT   DOMAIN    2597   2759       Laminin G-like 2.
FT   DOMAIN    2766   2926       Laminin G-like 3.
FT   DOMAIN    2986   3150       Laminin G-like 4.
FT   DOMAIN    3157   3330       Laminin G-like 5.
FT   DOMAIN    1854   1983       Coiled coil (Potential).
FT   DOMAIN    2015   2060       Coiled coil (Potential).
FT   DOMAIN    2091   2168       Coiled coil (Potential).
FT   DOMAIN    2214   2241       Coiled coil (Potential).
FT   DOMAIN    2321   2386       Coiled coil (Potential).
FT   SITE      2277   2279       Cell attachment site (Potential).
FT   DISULFID  1310   1317       By similarity.
FT   DISULFID  1312   1324       By similarity.
FT   DISULFID  1326   1335       By similarity.
FT   DISULFID  1338   1351       By similarity.
FT   DISULFID  1354   1369       By similarity.
FT   DISULFID  1356   1376       By similarity.
FT   DISULFID  1378   1387       By similarity.
FT   DISULFID  1390   1401       By similarity.
FT   DISULFID  1404   1416       By similarity.
FT   DISULFID  1406   1423       By similarity.
FT   DISULFID  1425   1434       By similarity.
FT   DISULFID  1437   1452       By similarity.
FT   DISULFID  1687   1696       By similarity.
FT   DISULFID  1689   1703       By similarity.
FT   DISULFID  1706   1715       By similarity.
FT   DISULFID  1718   1731       By similarity.
FT   DISULFID  1734   1746       By similarity.
FT   DISULFID  1736   1755       By similarity.
FT   DISULFID  1757   1766       By similarity.
FT   DISULFID  1769   1784       By similarity.
FT   DISULFID  1822   1822       Interchain (Probable).
FT   DISULFID  1825   1825       Interchain (Probable).

  Query Match             92.0%;  Score 2704;  DB 1;  Length 3333;
  Best Local Similarity   92.2%;  Pred. No. 8.3e-175;
  Matches  521;  Conservative   15;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2390 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 2449

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||| |||||||||||||||||||||| ||||||||||||||||||||||
Db       2450 MAVVDGQLTCVYNLGDGEAEVQIDQVLTESESQEAVMDRVKSQRIYQFAKLNYTKEATST 2509

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||||| |||:|  |||||||||||:|||||||||| |||| ||||||||||||||||||||
Db       2510 KPKAPGVYDMESASSNTLLNLDPENAVFYVGGYPPGFELPRRLRFPPYKGCIELDDLNEN 2569

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2570 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPKLSWTIQTTV 2629

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              ||||||||||||||||||||||:|||||||||||||||||:|:|| |||:||| |
Db       2630 DRGLLFFAENQDNFISLNIEDGNLMVKYKLNSEPPKEKGIRDTINNGRDHMILISIGKSQ 2689

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              ||| ||:|: |: |||||||||||||||||||||| :|||||||||||||||||||||||
Db       2690 KRMLINMNKHSIIIEGEIFDFSTYYLGGIPIAIRERFPLSTPAFQGCMKNLKKTSGVVRL 2749

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2750 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSLDRFQLSFGFQTFQPSGTLLNHQ 2809

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              |||||||||||||| ||||||: |||||||||||||||||||||||||||||||||||||
Db       2810 TRTSSLLVTLEDGHIALSTRDSSSPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 2869

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ||||| ||||||||| :|||:|||||||| ||| |||||||:||||||:|| |||||||
Db       2870 RNQRLASFSNAQQSLSMGGGYFEGCISNVFVQRMSQSPEVLDMASKSTKRDAFLGGCSLN 2929

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              |||||||||||| ||| | ||||||
Db       2930 KPPFLMLFKSPKGFNKARSFNVNQL 2954


RESULT 3
Q6VU69
ID   Q6VU69      PRELIMINARY;      PRT;  1668 AA.
AC   Q6VU69;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
```

```
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Laminin alpha 3 splice variant a.
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
RA   McLean W.H., Irvine A.D., Hamill K.J., Whittock N.V.,
RA   Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
RA   Dopping-Hepenstal P.J., Eady R.A., Jamil T., Phillips R.J.,
RA   Shabbir S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
RA   Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
RA   McGrath J.A.;
RT   "An unusual N-terminal deletion of the laminin {alpha}3a isoform leads
RT   to the chronic granulation tissue disorder laryngo-onycho-cutaneous
RT   syndrome.";
RL   Hum. Mol. Genet. 12:2395-2409(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   McLean W.H.I.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY327114; AAQ72569.1; -.
DR   GO; GO:0005606; C:laminin-1; IEA.
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002049; LamInin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00053; Laminin_EGF; 1.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   SMART; SM00180; EGF_Lam; 2.
DR   SMART; SM00282; LamG; 5.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Laminin EGF-like domain.
SQ   SEQUENCE   1668 AA;  184053 MW;  9EBF5FC45637645C CRC64;

  Query Match           83.0%;  Score 2441;  DB 2;  Length 1668;
  Best Local Similarity   81.9%;  Pred. No. 2.7e-157;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||: |||||||:|||||||||||||:||||
Db        726 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 785

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        786 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 845

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db        846 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 905

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| |||||||||||||||||||||||||||:||||:|| | | |||||||
Db        906 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 965

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db        966 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1025

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||:||||||||||||||
Db       1026 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1085

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:|||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1086 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1145

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| |||||:|||||  ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1146 TWTRNLQVTLEDGYIELSTSDSGSPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1205

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1206 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1265

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1266 KPPFLMLLKGSTRFNKTKTFRINQL 1290


RESULT 4
Q6VU67
ID   Q6VU67      PRELIMINARY;      PRT;  3277 AA.
AC   Q6VU67;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Laminin alpha 3 splice variant b2.
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
RA   McLean W.H., Irvine A.D., Hamill K.J., Whittock N.V.,
RA   Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
RA   Dopping-Hepenstal P.J., Eady R.A., Jamil T., Phillips R.J.,
RA   Shabbir S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
RA   Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
RA   McGrath J.A.;
RT   "An unusual N-terminal deletion of the laminin {alpha}3a isoform leads
RT   to the chronic granulation tissue disorder laryngo-onycho-cutaneous
RT   syndrome.";
RL   Hum. Mol. Genet. 12:2395-2409(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   McLean W.H.I.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY327116; AAQ72571.1; -.
DR   GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR   GO; GO:0005606; C:laminin-1; IEA.
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
```

```
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR008211; Laminin_N.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 8.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   Pfam; PF00055; Laminin_N; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   ProDom; PD003031; Laminin_B; 1.
DR   SMART; SM00181; EGF; 8.
DR   SMART; SM00180; EGF_Lam; 14.
DR   SMART; SM00281; LamB; 1.
DR   SMART; SM00282; LamG; 5.
DR   SMART; SM00136; LamNT; 1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; 12.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 13.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Laminin EGF-like domain.
SQ   SEQUENCE   3277 AA;  360209 MW;  3ACFFE998357122E CRC64;

  Query Match           83.0%;  Score 2441;  DB 2;  Length 3277;
  Best Local Similarity   81.9%;  Pred. No. 6.9e-157;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||||||||||||: |||||||:|||||||||||:||||
Db       2335 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 2394

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              |||||||||||||||||||:|:||:||:||::|||||||||||||||:|||||  |||:
Db       2395 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 2454

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRPPPYKGCIELDDLNEN 180
              ||: | |||::| :||||||||||: ||||||||||:|||||  ||||||||||||||||
Db       2455 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 2514

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db       2515 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 2574

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       2575 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 2634

Qy        301 KRMWINVVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||:|||||||||||||||||
Db       2635 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 2694

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:|||||||:|||:| :| ||  | ||||||||||| ||:||
Db       2695 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 2754

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       2755 TWTRNLQVTLEDGYIELSTSDSGSPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 2814

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       2815 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 2874

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       2875 KPPFLMLLKGSTRFNKTKTFRINQL 2899


RESULT 5
Q6VU68
ID   Q6VU68      PRELIMINARY;      PRT;  3333 AA.
AC   Q6VU68;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Laminin alpha 3 splice variant b1.
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
RA   McLean W.H., Irvine A.D., Hamill K.J., Whittock N.V.,
RA   Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
RA   Dopping-Hepenstal P.J., Eady R.A., Jamil T., Phillips R.J.,
RA   Shabbir S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
RA   Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
RA   McGrath J.A.;
RT   "An unusual N-terminal deletion of the laminin {alpha}3a isoform leads
RT   to the chronic granulation tissue disorder laryngo-onycho-cutaneous
RT   syndrome.";
RL   Hum. Mol. Genet. 12:2395-2409(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   McLean W.H.I.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY327115; AAQ72570.1; -.
DR   GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR   GO; GO:0005606; C:laminin-1; IEA.
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR008211; Laminin_N.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 8.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   Pfam; PF00055; Laminin_N; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   ProDom; PD003031; Laminin_B; 1.
DR   SMART; SM00181; EGF; 8.
DR   SMART; SM00180; EGF_Lam; 14.
DR   SMART; SM00281; LamB; 1.
DR   SMART; SM00282; LamG; 5.
DR   SMART; SM00136; LamNT; 1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; 12.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 13.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Laminin EGF-like domain.
SQ   SEQUENCE   3333 AA;  366646 MW;  9F99AF49B8EF27DD CRC64;

  Query Match           83.0%;  Score 2441;  DB 2;  Length 3333;
  Best Local Similarity   81.9%;  Pred. No. 7.1e-157;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||||||||||||: |||||||:|||||||||||:||||
```

```
Db       2391 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 2450

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||:|:||:||:||::||||||||||||||:||||| |||:
Db       2451 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 2510

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db       2511 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 2570

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db       2571 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 2630

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       2631 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 2690

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||:|||||||||||||||
Db       2691 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 2750

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       2751 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 2810

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| |||||||:|||||| ||||||||||:||
Db       2811 TWTRNLQVTLEDGYIELSTSDSGSPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 2870

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::||||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       2871 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 2930

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       2931 KPPFLMLLKGSTRFNKTKTFRINQL 2955


RESULT 6
LMA3_HUMAN
ID   LMA3_HUMAN     STANDARD;      PRT;  1713 AA.
AC   Q16787; Q13679; Q13680;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Laminin alpha-3 chain precursor (Epiligrin 170 kDa subunit) (E170)
DE   (Nicein alpha subunit).
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Keratinocytes;
RX   MEDLINE=94357926; PubMed=8077230;
RA   Ryan M.C., Tizard R., Vandevanter D.R., Carter W.G.;
RT   "Cloning of the LamA3 gene encoding the alpha 3 chain of the adhesive
RT   ligand epiligrin. Expression in wound repair.";
RL   J. Biol. Chem. 269:22779-22787(1994).
RN   [2]
RP   SEQUENCE OF 1-1331 FROM N.A. (ISOFORMS A AND B).
RX   MEDLINE=96163880; PubMed=8586427;
RA   Vidal F., Baudoin C., Miquel C., Galliano M.-F., Christiano A.M.,
RA   Uitto J., Ortonne J.-P., Meneguzzi G.;
RT   "Cloning of the laminin alpha 3 chain gene (LAMA3) and identification
RT   of a homozygous deletion in a patient with Herlitz junctional
RT   epidermolysis bullosa.";
RL   Genomics 30:273-280(1995).
RN   [3]
RP   DISEASE.
RX   PubMed=12915477; DOI=10.1093/hmg/ddg234;
RA   Irwin McLean W.H., Irvine A.D., Hamill K.J., Whittock N.V.,
RA   Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
RA   Dopping-Hepenstal P.J.H., Eady R.A.J., Jamil T., Phillips R.J.,
RA   Shabbir S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
RA   Darling J., Atherton D.J., Van Steensel M.A.M., Munro C.S.,
RA   Smith F.J.D., McGrath J.A.;
RT   "An unusual N-terminal deletion of the laminin alpha3a isoform leads
RT   to the chronic granulation tissue disorder laryngo-onycho-cutaneous
RT   syndrome.";
RL   Hum. Mol. Genet. 12:2395-2409(2003).
CC   -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC       is thought to mediate the attachment, migration and organization
CC       of cells into tissues during embryonic development by interacting
CC       with other extracellular matrix components.
CC   -!- FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
CC       via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-
CC       6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine
CC       phosphorylation of pp125-FAK and p80, (3) differentiation of
CC       keratinocytes.
CC   -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC       different polypeptide chains (alpha, beta, gamma), which are bound
CC       to each other by disulfide bonds into a cross-shaped molecule
CC       comprising one long and three short arms with globules at each
CC       end. The alpha-3 chain is a subunit of laminin-5
CC       (epiligrin/kalinin/nicein), and possibly also a component of
CC       laminin-6 (K-laminin) and laminin-7 (KS-laminin).
CC   -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC       membranes (major component).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=A;
CC         IsoId=Q16787-1; Sequence=Displayed;
CC       Name=B;
CC         IsoId=Q16787-2; Sequence=VSP_003037;
CC         Note=Incomplete sequence;
CC   -!- TISSUE SPECIFICITY: Skin; respiratory, urinary, and digestive
CC       epithelia and in other specialized tissues with prominent
CC       secretory or protective functions. Epithelial basement membrane,
CC       and epithelial cell tongue that migrates into a wound bed. A
CC       differential and focal expression of the alpha-3 chain is observed
CC       in the CNS.
CC   -!- INDUCTION: Laminin-5 is up-regulated in wound sites of human skin.
CC   -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC       with other laminin chains to form a coiled coil structure.
CC   -!- DOMAIN: Domain G is globular.
CC   -!- DISEASE: Defects in LAMA3 are a cause of junctional epidermolysis
CC       bullosa gravis (JEB) [MIM:226700]; also known as junctional
CC       epidermolysis bullosa Herlitz-Pearson type. JEB is a blistering
CC       disorder in skin that is characterized by a separation of basal
CC       cells from the basement membrane due to a decreased number of
CC       hemidesmosomes. Laminin-5 is missing from the basement membrane of
CC       patients with the gravis form of epidermolysis bullosa.
CC   -!- DISEASE: Defects in LAMA3 are the cause of laryngoonychocutaneous
CC       syndrome (LOCS) [MIM:245660]. LOCS is an autosomal recessive
CC       epithelial disorder confined to the Punjabi Muslim population. The
CC       condition is characterized by cutaneous erosions, nail dystrophy
CC       and exuberant vascular granulation tissue in certain epithelia,
CC       especially conjunctiva and larynx.
CC   -!- SIMILARITY: Contains 3 laminin EGF-like domains.
CC   -!- SIMILARITY: Contains 5 laminin G-like domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L34155; AAA59483.1; -.
DR   EMBL; X85107; CAA59428.1; -.
DR   EMBL; X85108; CAA59429.1; -.
DR   PIR; A55347; A55347.
```

```
DR   HSSP; P02468; 1NPE.
DR   Genew; HGNC:6483; LAMA3.
DR   MIM; 600805; -.
DR   MIM; 226700; -.
DR   MIM; 245660; -.
DR   GO; GO:0005604; C:basement membrane; TAS.
DR   GO; GO:0008544; P:epidermal differentiation; TAS.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00053; Laminin_EGF; 2.
DR   Pfam; PF00054; Laminin_G; 2.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Alternative splicing; Basement membrane; Cell adhesion; Coiled coil;
KW   Epidermolysis bullosa; Extracellular matrix; Glycoprotein;
KW   Laminin EGF-like domain; Repeat; Signal.
FT   SIGNAL       1    20       Potential.
FT   CHAIN       21  1713       Laminin alpha-3 chain.
FT   DOMAIN      46   201       Domain III A.
FT   DOMAIN      67   113       Laminin EGF-like 1.
FT   DOMAIN     114   166       Laminin EGF-like 2.
FT   DOMAIN     167   185       Laminin EGF-like 3 (incomplete).
FT   DOMAIN     186   769       Domain II and I.
FT   DOMAIN     770   971       Laminin G-like 1.
FT   DOMAIN     978  1140       Laminin G-like 2.
FT   DOMAIN    1147  1307       Laminin G-like 3.
FT   DOMAIN    1366  1530       Laminin G-like 4.
FT   DOMAIN    1537  1710       Laminin G-like 5.
FT   DOMAIN     231   327       Coiled coil (Potential).
FT   DOMAIN     396   548       Coiled coil (Potential).
FT   DOMAIN     594   621       Coiled coil (Potential).
FT   DOMAIN     702   765       Coiled coil (Potential).
FT   DOMAIN    1686  1713       Coiled coil (Potential).
FT   DISULFID    67    76       By similarity.
FT   DISULFID    69    83       By similarity.
FT   DISULFID    86    95       By similarity.
FT   DISULFID    98   111       By similarity.
FT   DISULFID   114   126       By similarity.
FT   DISULFID   116   135       By similarity.
FT   DISULFID   137   146       By similarity.
FT   DISULFID   149   164       By similarity.
FT   DISULFID   202   202       Interchain (Probable).
FT   DISULFID   205   205       Interchain (Probable).
FT   SITE       658   660       Cell attachment site (Potential).
FT   CARBOHYD   542   542       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   645   645       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   745   745       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   882   882       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   964   964       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1108  1108       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1131  1131       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1325  1325       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1477  1477       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1667  1667       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC     1    45       MGWLWIFGAALGQCLGYSSQQQRVPFLQPPGQSQLQASYVE
FT                              FRPS -> KVSSYGGYLTYQAKSFALPGDMVLLEKKPDVQL
FT                              TGQHMSIIYEETNTPRPDRLHHGRVHVVEGNFRHASSRAPV
FT                              SREELMTVLSRLADVRIQGLYFTETQRLTLSEVGLEEASDT
FT                              GSGRIALAVEICACPPAYAGDSC (in isoform B).
FT                              /FTId=VSP_003037.
FT   CONFLICT     5     5       W -> R (in Ref. 2).
FT   CONFLICT   123   125       ATG -> GMC (in Ref. 2).
FT   CONFLICT   481   481       M -> K (in Ref. 2).
FT   CONFLICT   754   754       R -> L (in Ref. 2).
FT   CONFLICT   969   969       E -> Q (in Ref. 2).
FT   CONFLICT  1052  1052       D -> A (in Ref. 2).
FT   CONFLICT  1184  1184       G -> A (in Ref. 2).
SQ   SEQUENCE  1713 AA;  189304 MW;  45EA9BE1017B60D3 CRC64;

  Query Match             83.0%;  Score 2439;  DB 1;  Length 1713;
  Best Local Similarity   81.9%;  Pred. No. 3.8e-157;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| |||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||| ||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDPSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||||:||||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDPSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| |||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ::||   |:::||||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 7
Q96TG0
ID   Q96TG0      PRELIMINARY;      PRT;  1806 AA.
AC   Q96TG0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Alpha 3B chain of laminin-5 (Fragment).
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Aberdam D., Vidal, Baudoin, Miquel, Ortonne, Meneguzzi;
RL   Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X84900; CAA59325.1; -.
DR   HSSP; P02468; 1NPE.
DR   GO; GO:0005606; C:laminin-1; IEA.
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
```

```
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 2.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   ProDom; PD003031; Laminin_B; 1.
DR   SMART; SM00180; EGF_Lam; 2.
DR   SMART; SM00281; LamB; 1.
DR   SMART; SM00282; LamG; 5.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; 2.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Laminin EGF-like domain.
FT   NON_TER       1      1
SQ   SEQUENCE   1806 AA;  199411 MW;  EF94CDE2AEA52B93 CRC64;

  Query Match             83.0%;  Score 2439;  DB 2;  Length 1806;
  Best Local Similarity   81.9%;  Pred. No. 4.1e-157;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||: |||||||:|||||||||||||:||||
Db        864 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 923

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        924 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 983

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db        984 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 1043

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||:||||:|| | | |||||||
Db       1044 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1103

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | ||||
Db       1104 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1163

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||:|||||||||||||||
Db       1164 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1223

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | |||||||||||| ||:||
Db       1224 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1283

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:|||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1284 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1343

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1344 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1403

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1404 KPPFLMLLKGSTRFNKTKTFRINQL 1428
```

```
RESULT 8
Q76E14
ID   Q76E14      PRELIMINARY;      PRT;  3333 AA.
AC   Q76E14;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Laminin alpha 3b chain.
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kariya Y., Yasuda C., Nakashima Y., Ishida K., Tsubota Y.,
RA   Miyazaki K.;
RT   "Characterization of laminin 5B and NH2-terminal proteolytic fragment
RT   of its alpha3B chain: promotion of cellular adhesion, migration, and
RT   proliferation.";
RL   J. Biol. Chem. 279:24774-24784(2004).
DR   EMBL; AB107369; BAD13428.1; -.
DR   GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR   GO; GO:0005606; C:laminin-1; IEA.
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR008211; Laminin_N.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 8.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   Pfam; PF00055; Laminin_N; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   ProDom; PD003031; Laminin_B; 1.
DR   SMART; SM00181; EGF; 8.
DR   SMART; SM00180; EGF_Lam; 14.
DR   SMART; SM00281; LamB; 1.
DR   SMART; SM00282; LamG; 5.
DR   SMART; SM00136; LamNT; 1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; 12.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 13.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Laminin EGF-like domain.
SQ   SEQUENCE   3333 AA;  366616 MW;  6F99AF4D4B99FCB0 CRC64;

  Query Match             83.0%;  Score 2439;  DB 2;  Length 3333;
  Best Local Similarity   81.9%;  Pred. No. 9.7e-157;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||: |||||||:|||||||||||||:||||
Db       2391 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 2450

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
```

```
Db       2451 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 2510

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180

Db       2511 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 2570

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240

Db       2571 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 2630

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300

Db       2631 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 2690

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360

Db       2691 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 2750

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420

Db       2751 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 2810

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480

Db       2811 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 2870

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540

Db       2871 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 2930

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565

Db       2931 KPPFLMLLKGSTRFNKTKTFRINQL 2955


RESULT 9
Q867A1
ID   Q867A1      PRELIMINARY;      PRT;  1725 AA.
AC   Q867A1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Laminin alpha 3 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Spirito F., Capt A., Guaguere E., Ortonne J.-P., Meneguzzi G.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF236865; AAL54876.1; -.
DR   HSSP; P11209; 1G2C.
DR   GO; GO:0005606; C:laminin-1; IEA.
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00053; Laminin_EGF; 2.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   SMART; SM00180; EGF_Lam; 2.
DR   SMART; SM00282; LamG; 5.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Laminin EGF-like domain.
FT   NON_TER    1725   1725
SQ   SEQUENCE   1725 AA;  191053 MW;  DF71EB0E1FB5134C CRC64;

  Query Match             75.7%;  Score 2224.5;  DB 2;  Length 1725;
  Best Local Similarity   75.0%;  Pred. No. 1.6e-142;
  Matches  423;  Conservative   60;  Mismatches   80;  Indels    1;  Gaps    1;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60

Db        782 MRFNGKSGVEVRLPNDLEDLKGYTSLSFFLQRPESRESGRTENMFVMYLGNKDISRDYIG 841

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120

Db        842 MAVVDGRLTCVYNLGEQESESLQVDQSVIKSETQEAIMDRVKFQRIYQFASLNYTKKATSS 901

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180

Db        902 KPGSSQFHEMDSGNSHTLLNLDPENTVFYVGGYPSDFTLPARLRFPPYKGCIELDDLNEN 961

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240

Db        962 VLSLYNFKKTFNLNTTEVEPCRRRKEESDRNYFEGTGYARVPTQLNAPNPNFGLTIQTTV 1021

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300

Db       1022 DRGLLFFAENQDRFISLNIEDGKLLVQYKLNSEPPKEREIGHIVNDGKDHRILIVIGKFQ 1081

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360

Db       1082 NRISIAVSSQNSQIDGDIFDFSTYYLGGIPISIRERFNISTPAFRGCMKNLKKTTGVVRL 1141

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420

Db       1142 NDTVGVTKKCSEDWKLVRSASFSRDGQLRFTGLDLPLPSEFQASFGFQTFQPSGILFNLQ 1201

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480

Db       1202 SPKHYLQVTLEDGHIELNTRENSL-IIRSPQTYMDGELHFVSVIGDNSGLRLLIDDQTLK 1260

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540

Db       1261 SNQKLQDLSGSQHPLYLGGGSQFEGCISNVFIQRVSKSPAVLDLASKTFKRDVSLGGCSLN 1320

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQ 564

Db       1321 KPPFLMLLRGSTRLNKSHTFNINQ 1344


RESULT 10
LMA5_HUMAN
ID   LMA5_HUMAN     STANDARD;      PRT;  3695 AA.
AC   O15230; Q8WZA7; Q9H1P1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Laminin alpha-5 chain precursor.
GN   Name=LAMA5; Synonyms=KIAA0533, KIAA1907;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA   Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
```

```
RA   Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
RN   [2]
RP   SEQUENCE OF 197-1934 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21456161; PubMed=11572484;
RA   Nagase T., Kikuno R., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XXI.
RT   The complete sequences of 60 new cDNA clones from brain which code for
RT   large proteins.";
RL   DNA Res. 8:179-187(2001).
RN   [3]
RP   SEQUENCE OF 2051-3695 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98290545; PubMed=9628581;
RA   Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RA   Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. IX.
RT   The complete sequences of 100 new cDNA clones from brain which can
RT   code for large proteins in vitro.";
RL   DNA Res. 5:31-39(1998).
RN   [4]
RP   SEQUENCE OF 2743-3695 FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=97415425; PubMed=9271224; DOI=10.1016/S0014-5793(97)00686-8;
RA   Durkin M.E., Loechel F., Mattei M.-G., Gilpin B.J., Albrechtsen R.,
RA   Wewer U.M.;
RT   "Tissue-specific expression of the human laminin alpha5-chain, and
RT   mapping of the gene to human chromosome 20q13.2-13.3 and to distal
RT   mouse chromosome 2 near the locus for the ragged (Ra) mutation.";
RL   FEBS Lett. 411:296-300(1997).
RN   [5]
RP   EXPRESSION IN RETINA.
RX   MEDLINE=20422761; PubMed=10964957;
RA   Libby R.T., Champliaud M.-F., Claudepierre T., Xu Y., Gibbons E.P.,
RA   Koch M., Burgeson R.E., Hunter D.D., Brunken W.J.;
RT   "Laminin expression in adult and developing retinae: evidence of two
RT   novel CNS laminins.";
RL   J. Neurosci. 20:6517-6528(2000).
CC   -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC       is thought to mediate the attachment, migration and organization
CC       of cells into tissues during embryonic development by interacting
CC       with other extracellular matrix components.
CC   -!- SUBUNIT: Laminin-15 complex is an heterotrimer composed of three
CC       chains (alpha-5/beta-2/gamma-3) which are bound to each other by
CC       disulfide bonds into a cross-shaped molecule comprising one long
CC       and three short arms with globules at each end.
CC   -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC       membranes (major component).
CC   -!- TISSUE SPECIFICITY: Expressed in heart, lung, kidney, skeletal
CC       muscle, pancreas, retina and placenta. Little or no expression in
CC       brain and liver.
CC   -!- DOMAIN: Domain G is globular and is part of the major cell-binding
CC       site located in the long arm of the laminin heterotrimer.
CC   -!- SIMILARITY: Contains 22 laminin EGF-like domains.
CC   -!- SIMILARITY: Contains 5 laminin G-like domains.
CC   -!- SIMILARITY: Contains 2 laminin IV domains.
CC   -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AL354836; CAC22309.1; ALT_SEQ.
DR   EMBL; AL354836; CAC22310.1; -.
DR   EMBL; AB067494; BAB67800.1; -.
DR   EMBL; AB011105; BAA25459.1; -.
DR   EMBL; Z95636; CAB09137.1; -.
DR   HSSP; P02468; 1NPE.
DR   Genew; HGNC:6485; LAMA5.
DR   MIM; 601033; -.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR008211; Laminin_N.
DR   InterPro; IPR008212; Lam_N2.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 18.
DR   Pfam; PF00054; Laminin_G; 2.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   Pfam; PF00055; Laminin_N; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   ProDom; PD003031; Laminin_B; 1.
DR   PROSITE; PS00022; EGF_1; 19.
DR   PROSITE; PS01186; EGF_2; 3.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Basement membrane; Cell adhesion; Coiled coil; Extracellular matrix;
KW   Glycoprotein; Laminin EGF-like domain; Repeat; Signal.
FT   SIGNAL        1     35       Potential.
FT   CHAIN        36   3695       Laminin alpha-5 chain.
FT   DOMAIN       36    299       Laminin N-terminal (domain VI).
FT   DOMAIN      300    358       Laminin EGF-like 1.
FT   DOMAIN      359    428       Laminin EGF-like 2.
FT   DOMAIN      429    474       Laminin EGF-like 3.
FT   DOMAIN      494    540       Laminin EGF-like 4.
FT   DOMAIN      541    586       Laminin EGF-like 5.
FT   DOMAIN      587    631       Laminin EGF-like 6.
FT   DOMAIN      632    676       Laminin EGF-like 7.
FT   DOMAIN      677    722       Laminin EGF-like 8.
FT   DOMAIN      723    775       Laminin EGF-like 9.
FT   DOMAIN      776    828       Laminin EGF-like 10.
FT   DOMAIN      829    850       Laminin EGF-like 11 (incomplete).
FT   DOMAIN      851   1437       Laminin domain IV 1 (domain IV B).
FT   DOMAIN     1438   1483       Laminin EGF-like 12.
FT   DOMAIN     1484   1527       Laminin EGF-like 13.
FT   DOMAIN     1528   1576       Laminin EGF-like 14.
FT   DOMAIN     1577   1627       Laminin EGF-like 15.
FT   DOMAIN     1628   1637       Laminin EGF-like 16 (N-terminal).
FT   DOMAIN     1638   1830       Laminin domain IV 2 (domain IV A).
FT   DOMAIN     1831   1863       Laminin EGF-like 16 (C-terminal).
FT   DOMAIN     1864   1912       Laminin EGF-like 17.
FT   DOMAIN     1913   1968       Laminin EGF-like 18.
```

```
FT   DOMAIN     1969   2022       Laminin EGF-like 19.
FT   DOMAIN     2023   2069       Laminin EGF-like 20.
FT   DOMAIN     2070   2116       Laminin EGF-like 21.
FT   DOMAIN     2117   2166       Laminin EGF-like 22.
FT   DOMAIN     2167   2735       Domain II and I.
FT   DOMAIN     2736   2929       Laminin G-like 1.
FT   DOMAIN     2941   3115       Laminin G-like 2.
FT   DOMAIN     3124   3292       Laminin G-like 3.
FT   DOMAIN     3340   3513       Laminin G-like 4.
FT   DOMAIN     3520   3692       Laminin G-like 5.
FT   DOMAIN     2203   2221       Coiled coil (Potential).
FT   DOMAIN     2335   2466       Coiled coil (Potential).
FT   DOMAIN     2510   2670       Coiled coil (Potential).
FT   SITE       1722   1724       Cell attachment site (Potential).
FT   SITE       1838   1840       Cell attachment site (Potential).
FT   DISULFID    300    309       By similarity.
FT   DISULFID    302    322       By similarity.
FT   DISULFID    324    333       By similarity.
FT   DISULFID    336    356       By similarity.
FT   DISULFID    359    368       By similarity.
FT   DISULFID    361    393       By similarity.
FT   DISULFID    396    405       By similarity.
FT   DISULFID    408    426       By similarity.
FT   DISULFID    429    440       By similarity.
FT   DISULFID    431    447       By similarity.
FT   DISULFID    449    458       By similarity.
FT   DISULFID    461    471       By similarity.
FT   DISULFID    494    506       By similarity.
FT   DISULFID    496    515       By similarity.
FT   DISULFID    517    526       By similarity.
FT   DISULFID    529    538       By similarity.
FT   DISULFID    541    553       By similarity.
FT   DISULFID    543    560       By similarity.
FT   DISULFID    562    571       By similarity.
FT   DISULFID    574    584       By similarity.
FT   DISULFID    587    599       By similarity.

  Query Match           24.2%;  Score 712;  DB 1;  Length 3695;
  Best Local Similarity  33.1%;  Pred. No. 6.4e-39;
  Matches  194;  Conservative   96;  Mismatches  214;  Indels   82;  Gaps   21;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |:|||:|||::| | || ||  ||:|  :|| |:     |||| ||||:|:: |: ||:|
Db       2737 MKFNGRSGVQLRTPRDLADLAAYTALKFYLQGPEPEPGQGTEDRFVMYMGSRQATGDYMG 2796

Qy         61 MAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE--- 116
              ::: | ::  || ||:   | : ||: : |          |  |  ||  :: | |
Db       2797 VSLRDKKVHWVYQLGEAGPAVLSIDEDIGEQ------FAAVSLDRTLQFGHMSVTVERQM 2850

Qy        117 --ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIEL 174
                |      ||     ||     |||| |:| ||||||||  |  |  |||| |:||||:
Db       2851 IQETKGDTVAPGA---EG-----LLNLRPDDFVFYVGGYPSTFTPPPLLRFPGYRGCIEM 2902

Qy        175 DDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPN-AP 228
              | ||| |:|||||: || |:|    || | |       :| :| :|||:|||      :
Db       2903 DTLNEEVVSLYNFERTFQLDTAVDRPCARSKSTGDPWLTDGSYLDGTGFARISFDSQIST 2962

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPP----- 275
              | | ::     |:||| : |  |: | :::|:|:: |  :         :||
Db       2963 TKRFEQELRLVSYSGVLFFLKQQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPPLTS 3022

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNER---SVRIEGEIFDFSTYYLGGI--- 329
              |:|:          :  :|  :||: : |      ||  : ::     |||||:
Db       3023 ASKAIQ----------VFLLGGSRKRVLVRVERATVYSVEQDNDLELADAYYLGGVPPD 3071

Qy        330 --PIAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSR 384
                | ::|  |  :  : :||:| :|   |   : ||| | ||:  |: |  : |  :|
Db       3072 QLPPSLRWLFP-TGGSVRGCVKGIKALGKYVDLKRLN-TTGVSAGCTADLLVGRAMTFHG 3129

Qy        385 GG--QMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDS 442
               |  ::: :|:  | |       ||| : | |  |     :       |:|: | : |    :
Db       3130 HGFLRLALSNV-APLTGNVYSGFGFHSAQDSALLYYRASPDGLCQVSLQQGRVSLQLLRT 3188

Qy        443 NIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQV--LRRNQRLPSFSNAQQS----LR 496
              :   |:   : ||  |:|:  |: :|: | :|||:  :: ::  |      |      |
Db       3189 EV---KTQAGFADGAPHYVAFYSNATGVWLYVDDQLQQMKPHRGPPPELQPQPEGPPRLL 3245

Qy        497 LGG-------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLG 535
               |||        :| |||||| |||       | ||       : | |
Db       3246 LGGLPESGTIYNFSGCISNVFVQRLLGPQRVFDLQQNLGSVNVSTG 3291


RESULT 11
Q8TDF8
ID   Q8TDF8      PRELIMINARY;      PRT;  3695 AA.
AC   Q8TDF8;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Laminin alpha5 chain precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21935381; PubMed=11821406; DOI=10.1074/jbc.M111228200;
RA   Doi M., Thyboll J., Kortesmaa J., Jansson K., Iivanainen A.,
RA   Parvardeh M., Timpl R., Hedin U., Swedenborg J., Tryggvason K.;
RT   "Recombinant human laminin-10 (alpha5beta1gamma1). Production,
RT   purification, and migration-promoting activity on vascular endothelial
RT   cells.";
RL   J. Biol. Chem. 277:12741-12748(2002).
DR   EMBL; AF443072; AAM12527.1; -.
DR   HSSP; P02468; 1NPE.
DR   GO; GO:0005605; C:basal lamina; NAS.
DR   GO; GO:0005178; F:integrin binding; IDA.
DR   GO; GO:0005198; F:structural molecule activity; IC.
DR   GO; GO:0001525; P:angiogenesis; NAS.
DR   GO; GO:0016477; P:cell migration; IDA.
DR   GO; GO:0008283; P:cell proliferation; NAS.
DR   GO; GO:0008037; P:cell recognition; NAS.
DR   GO; GO:0007010; P:cytoskeleton organization and biogenesis; NAS.
DR   GO; GO:0009790; P:embryonic development; NAS.
DR   GO; GO:0045446; P:endothelial cell differentiation; NAS.
DR   GO; GO:0048041; P:focal adhesion formation; NAS.
DR   GO; GO:0007229; P:integrin-mediated signaling pathway; IMP.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR008211; Laminin_N.
DR   InterPro; IPR001638; SBP_bac_3.
DR   InterPro; IPR001368; TNFR_c6.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 20.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   Pfam; PF00055; Laminin_N; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   ProDom; PD003031; Laminin_B; 1.
DR   SMART; SM00180; EGF_Lam; 20.
DR   SMART; SM00281; LamB; 1.
DR   SMART; SM00282; LamG; 5.
DR   SMART; SM00136; LamNT; 1.
DR   PROSITE; PS00022; EGF_1; 19.
DR   PROSITE; PS01186; EGF_2; 3.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
```

```
DR   PROSITE; PS01039; SBP_BACTERIAL_3; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Laminin EGF-like domain; Signal.
FT   SIGNAL        1     35       Potential.
FT   CHAIN        36   3695       laminin alpha5 chain.
SQ   SEQUENCE   3695 AA;  399645 MW;  69703B52536EF0A3 CRC64;

  Query Match             24.2%;  Score 712;  DB 2;  Length 3695;
  Best Local Similarity   33.1%;  Pred. No. 6.4e-39;
  Matches  194;  Conservative   96;  Mismatches  214;  Indels   82;  Gaps   21;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |:|||:|||::| | || ||  ||:|  :|| |:     |||| ||||:|:: |: ||:|
Db       2737 MKFNGRSGVQLRTPRDLADLAAYTALKFYLQGPEPEPGQGTEDRFVMYMGSRQATGDYMG 2796

Qy         61 MAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE--- 116
              ::: | ::  || ||:   | : ||: : |          |   |  ||  :: | |
Db       2797 VSLRDKKVHWVYQLGEAGPAVLSIDEDIGEQ------FAAVSLDRTLQFGHMSVTVERQM 2850

Qy        117 --ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIEL 174
                |      ||     ||      |||| |:| |||||||  |  |  |||| |:||||:
Db       2851 IQETKGDTVAPGA---EG-----LLNLRPDDFVFYVGGYPSTFTPPPLLRFPGYRGCIEM 2902

Qy        175 DDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPN-AP 228
              | ||| |:|||||: || |:|    || | |       :| :| :|||:|||      :
Db       2903 DTLNEEVVSLYNFERTFQLDTAVDRPCARSKSTGDPWLTDGSYLDGTGFARISFDSQIST 2962

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPP----- 275
              | | ::     |:||| : |  |: | :::|:|:: |   :        :||
Db       2963 TKRFEQELRLVSYSGVLFFLKQQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPPLTS 3022

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNER---SVRIEGEIFDFSTYYLGGI--- 329
              | |:          :  :|  :||: : |      ||  : ::     |||||:
Db       3023 ASKAIQ----------VFLLGGSRKRVLVRVERATVYSVEQDNDLELADAYYLGGVPPD 3071

Qy        330 --PIAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSR 384
                | ::|  |  :  : :||:| :|    |   : ||| | ||:  |: |  : |  :|
Db       3072 QLPPSLRWLFP-TGGSVRGCVKGIKALGKYVDLKRLN-TTGVSAGCTADLLVGRAMTFHG 3129

Qy        385 GG--QMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDS 442
               |  ::: :|:  | |       ||| : | |  |     :      |:|: | : |    :
Db       3130 HGFLRLALSNV-APLTGNVYSGFGFHSAQDSALLYYRASPDGLCQVSLQQGRVSLQLLRT 3188

Qy        443 NIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQV--LRRNQRLPSFSNAQQS----LR 496
              :   |:   : ||  |:|:  |: :|: | :|||:  :: ::  |      |      |
Db       3189 EV---KTQAGFADGAPHYVAFYSNATGVWLYVDDQLQQMKPHRGPPPELQPQPEGPPRLL 3245

Qy        497 LGG-------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLG 535
              |||       :| |||||| |||      | ||      : | |
Db       3246 LGGLPESGTIYNFSGCISNVFVQRLLGPQRVFDLQQNLGSVNVSTG 3291


RESULT 12
LMA4_HUMAN
ID   LMA4_HUMAN     STANDARD;      PRT;  1816 AA.
AC   Q16363; Q14735; Q15335; Q9UE18; Q9UJN9;
DT   01-NOV-1997 (Rel. 35, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Laminin alpha-4 chain precursor.
GN   Name=LAMA4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal lung;
RX   MEDLINE=95300971; PubMed=7781776; DOI=10.1016/0014-5793(95)00462-I;
RA   Iivanainen A., Sainio K., Sariola H., Tryggvason K.;
RT   "Primary structure and expression of a novel human laminin alpha 4
RT   chain.";
RL   FEBS Lett. 365:183-188(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=97454279; PubMed=9310354;
RA   Richards A.J., Luccarini C., Pope F.M.;
RT   "The structural organisation of LAMA4, the gene encoding laminin
RT   alpha4.";
RL   Eur. J. Biochem. 248:15-23(1997).
RN   [3]
RP   SEQUENCE OF 236-1816 FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=95048381; PubMed=7959779;
RA   Richards A.J., Al-Imara L., Carter N.P., Lloyd J.C., Leversha M.A.,
RA   Pope F.M.;
RT   "Localization of the gene (LAMA4) to chromosome 6q21 and isolation of
RT   a partial cDNA encoding a variant laminin A chain.";
RL   Genomics 22:237-239(1994).
RN   [4]
RP   SEQUENCE OF 66-1816 FROM N.A.
RA   Tubby B.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC       is thought to mediate the attachment, migration and organization
CC       of cells into tissues during embryonic development by interacting
CC       with other extracellular matrix components.
CC   -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC       different polypeptide chains (alpha, beta, gamma), which are bound
CC       to each other by disulfide bonds into a cross-shaped molecule
CC       comprising one long and three short arms with globules at each
CC       end.
CC   -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC       membranes (major component).
CC   -!- TISSUE SPECIFICITY: In adult, strong expression in heart, lung,
CC       ovary small and large intestines, placenta, liver; weak or no
CC       expression in skeletal muscle, kidney, pancreas, testis, prostate,
CC       brain. High expression in fetal lung and kidney. Expression in
CC       fetal and newborn tissues is observed in certain mesenchymal cells
CC       in tissues such as smooth muscle and dermis.
CC   -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC       with other laminin chains to form a coiled coil structure.
CC   -!- DOMAIN: Domain G is globular.
CC   -!- SIMILARITY: Contains 4 laminin EGF-like domains.
CC   -!- SIMILARITY: Contains 5 laminin G-like domains.
CC   -!- CAUTION: Gene LAMA4 was formerly called LAMA3.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S78569; AAB34635.1; -.
DR   EMBL; X91171; CAA62596.1; -.
DR   EMBL; Y14240; CAA74636.1; -.
DR   EMBL; X76939; CAA54258.1; -.
DR   EMBL; Z99289; -; NOT_ANNOTATED_CDS.
DR   PIR; S68960; S68960.
DR   HSSP; P02468; 1NPE.
DR   Genew; HGNC:6484; LAMA4.
DR   MIM; 600133; -.
DR   GO; GO:0005605; C:basal lamina; TAS.
DR   GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00053; Laminin_EGF; 3.
```

```
DR   Pfam; PF00054; Laminin_G; 3.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
KW   Basement membrane; Cell adhesion; Coiled coil; Extracellular matrix;
KW   Glycoprotein; Laminin EGF-like domain; Repeat; Signal.
FT   SIGNAL       1     24       Potential.
FT   CHAIN       25   1816       Laminin alpha-4 chain.
FT   DOMAIN      82    131       Laminin EGF-like 1.
FT   DOMAIN     132    186       Laminin EGF-like 2.
FT   DOMAIN     187    240       Laminin EGF-like 3.
FT   DOMAIN     241    255       Laminin EGF-like 4 (incomplete).
FT   DOMAIN     256    825       Domain II and I.
FT   DOMAIN     826   1028       Laminin G-like 1.
FT   DOMAIN    1040   1220       Laminin G-like 2.
FT   DOMAIN    1227   1395       Laminin G-like 3.
FT   DOMAIN    1462   1633       Laminin G-like 4.
FT   DOMAIN    1640   1813       Laminin G-like 5.
FT   DOMAIN     313    396       Coiled coil (Potential).
FT   DOMAIN     466    521       Coiled coil (Potential).
FT   DOMAIN     574    607       Coiled coil (Potential).
FT   DOMAIN     655    717       Coiled coil (Potential).
FT   DOMAIN     770    799       Coiled coil (Potential).
FT   SITE       717    719       Cell attachment site (Potential).
FT   DISULFID    82     91       By similarity.
FT   DISULFID    84     98       By similarity.
FT   DISULFID   101    110       By similarity.
FT   DISULFID   113    129       By similarity.
FT   DISULFID   132    146       By similarity.
FT   DISULFID   134    155       By similarity.
FT   DISULFID   157    166       By similarity.
FT   DISULFID   169    184       By similarity.
FT   DISULFID   187    202       By similarity.
FT   DISULFID   189    209       By similarity.
FT   DISULFID   212    221       By similarity.
FT   DISULFID   224    238       By similarity.
FT   DISULFID   266    266       Interchain (Probable).
FT   DISULFID   269    269       Interchain (Probable).
FT   CARBOHYD   104    104       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   215    215       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   308    308       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   458    458       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   524    524       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   550    550       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   571    571       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   574    574       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   631    631       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   639    639       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   735    735       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   751    751       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   754    754       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   780    780       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   803    803       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1086   1086       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1281   1281       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1359   1359       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1411   1411       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT   143    143       A -> P (in Ref. 1).
FT   CONFLICT   178    178       L -> F (in Ref. 1).
FT   CONFLICT   265    265       G -> GMDCPTIS (in Ref. 4).
FT   CONFLICT   276    276       D -> A (in Ref. 4).
FT   CONFLICT   491    491       Y -> H (in Ref. 2 and 3).
FT   CONFLICT  1057   1057       T -> P (in Ref. 1).
FT   CONFLICT  1110   1112       SGR -> GGP (in Ref. 4).
SQ   SEQUENCE  1816 AA;  201908 MW;  04E9AF379A0F4A4D CRC64;

  Query Match           23.3%;  Score 686;  DB 1;  Length 1816;
  Best Local Similarity  32.2%;  Pred. No. 1.4e-37;
  Matches  194;  Conservative  101;  Mismatches  245;  Indels   62;  Gaps   21;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFL----QRPDLRENGGTEDMFVMYLGNKDASK 56
              | |:|:| |||     ::||| :|||||::    :||:| |   | | |::|||:|:| |
Db        829 MMFDGQSAVEVHSRTSMDDLKAFTSLSLYMKPPVKRPELTE---TADQFILYLGSKNAKK 885

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
              :|:|:|: :  |  ||||| :: |: :|       |  |     || :|: :  |:  |
Db        886 EYMGLAIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVP 943

Qy        117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDD 176
              : |:  :   :   |    ::||:|||| |||||| | :|:||: |  | : ||:||
Db        944 SLSSTAEEKFIKKGEFSGDDSLLDLDPEDTVFYVGGVPSNFKLPTSLNLPGFVGCLELAT 1003

Qy        177 LNENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYA--RIPTQPN--A 227
              || :|:|||||  :|:: :   || | |       :   :|:|:|||  |  |:
Db       1004 LNNDVISLYNFKHIYNMDPSTSVPCARDKLAFTQSRAASYFFDGSGYAVVRDITRRGKFG 1063

Qy        228 PFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRY-------KLNSEPPKEKGI 280
                |   ::|  | |||:    |   |  | : :| | | |       ::: |   :|
Db       1064 QVTRFDIEVRTPADNGLILLMVNGSMFFRLEMRNGYLHVFYDFGFSSGRVHLEDTLKKA- 1122

Qy        281 RDTINDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIP------I 331
                ||| | | | | |    |:| : |: | |:    |     |:  |:|| |
Db       1123 --QINDAKYHEISI-IYHNDKKMILVVDRRHVKSMDNEKMKIPFTDIYIGGAPPEILQSR 1179

Qy        332 AIRERFNISTPAFQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQM 388
              |:|    :    |:|||     ||   ::   :|:||   | ||  : | | |:  ||
Db       1180 ALRAHLPLDI-NFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQS 1236

Qy        389 SFTNLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIF 447
                ::  :   | |:  | |:| ||:| |  : : :    ::|::| : :  :   | :
Db       1237 FIASIQKISFFDGFEGGFNFRTLQPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQ 1294

Qy        448 KSPGTYMDGLLHHVSVISDTSGLR--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-- 499
                | ||| |   ||| |  |  |::|  :|  :|         | |  :    ||
Db       1295 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSP 1352

Qy        500 -----GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
                  :| |||||    |  :  || |   : |   ||  | :   |  :| |  |
Db       1353 ISAQYANFTGCISNAYFTRVDRDVEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNL 1412

Qy        555 NK 556
              :|
Db       1413 SK 1414


RESULT 13
Q91VV0
ID   Q91VV0      PRELIMINARY;      PRT;  1254 AA.
AC   Q91VV0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Lama4 protein (Fragment).
GN   Name=Lama4;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
```

```
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC008533; AAH08533.1; -.
DR   HSSP; Q60675; 1QU0.
DR   MGD; MGI:109321; Lama4.
DR   GO; GO:0005605; C:basal lamina; IDA.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0001568; P:blood vessel development; IMP.
DR   Pfam; PF02210; Laminin_G_2; 5.
DR   Pfam; PF06009; Laminin_II; 1.
DR   SMART; SM00282; LamG; 5.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
FT   NON_TER       1      1
SQ   SEQUENCE   1254 AA;  139723 MW;  54D49EF763D37CD9 CRC64;

  Query Match           23.3%;  Score 685;  DB 2;  Length 1254;
  Best Local Similarity   32.2%;  Pred. No. 9.7e-38;
  Matches  193;  Conservative  100;  Mismatches  251;  Indels   56;  Gaps   20;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQ---RPDLRENGGTEDMFVMYLGNKDASKD 57
              | |:|:|  |||     ::||| :||:||:::   :|          | ||:|||:|:| |:
Db        267 MMFDGQSAVEVHPKVSVDDLKAFTSISLYMKPPPKPAEPTGAWVADQFVLYLGSKNAKKE 326

Qy         58 YIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEA 117
             |:|:|: :  |  |||||  :: |: :|       |  |     || :|: :  |:  |  :
Db        327 YMGLAIKNDNLVYVYNLGMKDVEILLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVPS 384

Qy        118 TSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDPELPSRLRFPPYKGCIELDDL 177
              |:  :   :   |    ::||:| ||| ||||||  | :|:||: |  | | ||:||  |
Db        385 LSSTAEEKFIKKGEFAGDDSLLDLTPEDTVFYVGGVPANFKLPASLNLPSYSGCLELATL 444

Qy        178 NENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYA--RIPTQPN--AP 228
              | :|:|||||  :|:: ::  || | |       :   :|:|: ||  |  |:
Db        445 NNDVISLYNFKHIYNMDPSKSVPCARDKLAFTQSRAASYFFDGSSYAVVRDITRRGKFGQ 504

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLN-SEPPKEKGIRDT---- 283
                |   |:|  | ||:    |   | || : :| | | |    | |    : ||
Db        505 VTRFDIEIRTPADNGLVLLMVNGSMFFSLEMRNGYLHVFYDFGFSNGPVH--LEDTLKKA 562

Qy        284 -INDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIPIAIRERFNI 339
              ||| | | | | |     |:| : |: | |:    | :   |:  |:|| |  : :   :
Db        563 QINDAKYHEISI-IYHNDKKMILVVDRRHVKSTDNEKKKIPFTDIYIGGAPQEVLQSRTL 621

Qy        340 STPA-----FQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFT 391
                 |:||||     ||   ::   :|:||   | ||  : | | |:  ||
Db        622 RAHLPLDINFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIA 679

Qy        392 NLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSP 450
              ::  :   | |:  | |:| ||:| |  : : :    ::|::| : :  :   | :  :
Db        680 SIQKISFFDGFEGGFNFRTLQPNGLLFYYTSGSDVFSISLDNGTVVMDVK--GIKVMSTD 737

Qy        451 GTYMDGLLHH-VSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQQS------LRLGG---- 499
              | ||| |  |: |||| |::|  ||    |:  |:|:          ||
Db        738 KQYHDGLPHFVVTSISDTR-YELVVDKSRLRGKN--PTKGKAEQTQTTEKKFYFGGSPIS 794

Qy        500 ---GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 556
                :| |||||    |  :  || |    | |   ||  | :   |  :| |  |  :|
Db        795 PQYANFTGCISNAYFTRLDRDVEVEDFQRYSEKVHTSLYECPIESSPLFLLHKKGKNSSK 854


RESULT 14
LMA4_MOUSE
ID   LMA4_MOUSE     STANDARD;      PRT;  1816 AA.
AC   P97927; O88785; P70409;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Laminin alpha-4 chain precursor.
GN   Name=Lama4;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 462-469; 478-483; 776-782 AND
RP   940-945.
RC   STRAIN=BALB/c; TISSUE=Endothelial cells;
RX   MEDLINE=97363207; PubMed=9219532;
RA   Frieser M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,
RA   Sorokin L.M.;
RT   "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of
RT   endothelium.";
RL   Eur. J. Biochem. 246:727-735(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=97202462; PubMed=9049981; DOI=10.1016/S0945-053X(96)90162-6;
RA   Liu J., Mayne R.;
RT   "The complete cDNA coding sequence and tissue-specific expression of
RT   the mouse laminin alpha 4 chain.";
RL   Matrix Biol. 15:433-437(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=98010627; PubMed=9346933; DOI=10.1074/jbc.272.44.27862;
RA   Iivanainen A., Kortesmaa J., Sahlberg C., Morita T., Bergmann U.,
RA   Thesleff I., Tryggvason K.;
RT   "Primary structure, developmental expression, and immunolocalization
RT   of the murine laminin alpha4 chain.";
RL   J. Biol. Chem. 272:27862-27868(1997).
RN   [4]
RP   SEQUENCE OF 836-1106 FROM N.A.
RC   STRAIN=ICR; TISSUE=Placenta;
RX   MEDLINE=97296337; PubMed=9151674; DOI=10.1083/jcb.137.3.685;
RA   Miner J.H., Patton B.L., Lentz S.I., Gilbert D.J., Snider W.D.,
RA   Jenkins N.A., Copeland N.G., Sanes J.R.;
RT   "The laminin alpha chains: expression, developmental transitions, and
RT   chromosomal locations of alpha1-5, identification of heterotrimeric
RT   laminins 8-11, and cloning of a novel alpha3 isoform.";
RL   J. Cell Biol. 137:685-702(1997).
RN   [5]
RP   SEQUENCE OF 1467-1691 FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=97187457; PubMed=9034910;
RX   DOI=10.1002/(SICI)1096-9861(19970224)378:4<547::AID-CNE9>3.0.CO;2-2;
RA   Lentz S.I., Miner J.H., Sanes J.R., Snider W.D.;
RT   "Distribution of the ten known laminin chains in the pathways and
RT   targets of developing sensory axons.";
RL   J. Comp. Neurol. 378:547-561(1997).
CC   -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC       is thought to mediate the attachment, migration and organization
CC       of cells into tissues during embryonic development by interacting
CC       with other extracellular matrix components.
CC   -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC       different polypeptide chains (alpha, beta, gamma), which are bound
CC       to each other by disulfide bonds into a cross-shaped molecule
CC       comprising one long and three short arms with globules at each
CC       end.
CC   -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC       membranes (major component).
CC   -!- TISSUE SPECIFICITY: Strongly expressed in peripheral nerves,
CC       cardiac muscle, fat, dermis, lung stroma, aortic endothelium,
CC       endocardium and endothelium of blood vessels in skin and brain.
CC   -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC       with other laminin chains to form a coiled coil structure.
```

```
CC   -!- DOMAIN: Domain G is globular.
CC   -!- SIMILARITY: Contains 4 laminin EGF-like domains.
CC   -!- SIMILARITY: Contains 5 laminin G-like domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U58950; AAB41840.1; -.
DR   EMBL; Y09827; CAA70970.1; -.
DR   EMBL; U59865; AAC24725.1; -.
DR   EMBL; U88352; AAC53178.1; -.
DR   EMBL; U69176; AAC52982.1; -.
DR   HSSP; P02468; 1NPE.
DR   MGD; MGI:109321; Lama4.
DR   GO; GO:0005604; C:basement membrane; IDA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00053; Laminin_EGF; 3.
DR   Pfam; PF00054; Laminin_G; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Basement membrane; Cell adhesion; Coiled coil;
KW   Direct protein sequencing; Extracellular matrix; Glycoprotein;
KW   Laminin EGF-like domain; Repeat; Signal.
FT   SIGNAL       1     24       Potential.
FT   CHAIN       25   1816       Laminin alpha-4 chain.
FT   DOMAIN      82    131       Laminin EGF-like 1.
FT   DOMAIN     132    186       Laminin EGF-like 2.
FT   DOMAIN     187    240       Laminin EGF-like 3.
FT   DOMAIN     241    255       Laminin EGF-like 4 (incomplete).
FT   DOMAIN     256    825       Domain II and I.
FT   DOMAIN     826   1030       Laminin G-like 1.
FT   DOMAIN    1042   1222       Laminin G-like 2.
FT   DOMAIN    1229   1397       Laminin G-like 3.
FT   DOMAIN    1462   1633       Laminin G-like 4.
FT   DOMAIN    1640   1813       Laminin G-like 5.
FT   DOMAIN     431    523       Coiled coil (Potential).
FT   DOMAIN     556    604       Coiled coil (Potential).
FT   DOMAIN     655    717       Coiled coil (Potential).
FT   DOMAIN     770    799       Coiled coil (Potential).
FT   SITE       717    719       Cell attachment site (Potential).
FT   DISULFID    82     91       By similarity.
FT   DISULFID    84     98       By similarity.
FT   DISULFID   101    110       By similarity.
FT   DISULFID   113    129       By similarity.
FT   DISULFID   132    146       By similarity.
FT   DISULFID   134    155       By similarity.
FT   DISULFID   157    166       By similarity.
FT   DISULFID   169    184       By similarity.
FT   DISULFID   187    202       By similarity.
FT   DISULFID   189    209       By similarity.
FT   DISULFID   212    221       By similarity.
FT   DISULFID   224    238       By similarity.
FT   DISULFID   266    266       Interchain (Probable).
FT   DISULFID   269    269       Interchain (Probable).
FT   CARBOHYD   104    104       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   215    215       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   308    308       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   333    333       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   458    458       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   550    550       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   571    571       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   574    574       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   631    631       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   639    639       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   735    735       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   751    751       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   754    754       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   780    780       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   803    803       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1088   1088       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1283   1283       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1361   1361       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT     8      8       C -> S (in Ref. 2).
FT   CONFLICT    18     18       C -> Y (in Ref. 2).
FT   CONFLICT   248    248       C -> R (in Ref. 3).
FT   CONFLICT   297    297       G -> A (in Ref. 3).
FT   CONFLICT   431    433       THR -> HPS (in Ref. 2).
FT   CONFLICT   679    679       S -> C (in Ref. 3).
FT   CONFLICT   703    703       D -> G (in Ref. 2).
FT   CONFLICT   706    706       N -> H (in Ref. 2).
FT   CONFLICT   728    728       K -> R (in Ref. 2).
FT   CONFLICT   730    730       F -> I (in Ref. 2).
FT   CONFLICT   779    779       R -> G (in Ref. 1; AA sequence).
FT   CONFLICT   810    810       R -> S (in Ref. 3).
FT   CONFLICT   865    867       AEP -> QT (in Ref. 2).
FT   CONFLICT   936    936       K -> E (in Ref. 3).
FT   CONFLICT   970    970       L -> V (in Ref. 3).
FT   CONFLICT  1132   1132       H -> R (in Ref. 2).
FT   CONFLICT  1200   1200       F -> I (in Ref. 2).
FT   CONFLICT  1382   1382       D -> A (in Ref. 2).
FT   CONFLICT  1413   1414       NS -> EF (in Ref. 1).
FT   CONFLICT  1489   1489       A -> S (in Ref. 2).
SQ   SEQUENCE   1816 AA;  201818 MW;  B49C45F3A45999D8 CRC64;

  Query Match           23.3%;  Score 685;  DB 1;  Length 1816;
  Best Local Similarity  32.2%;  Pred. No. 1.6e-37;
  Matches  193;  Conservative  100;  Mismatches  251;  Indels   56;  Gaps   20;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQ---RPDLRENGGTEDMFVMYLGNKDASKD 57
              | |:|:| |||     ::||| :||:||:::   :|        | ||:|||:|:| |:
Db        829 MMFDGQSAVEVHPKVSVDDLKAFTSISLYMKPPPKPAEPTGAWVADQFVLYLGSKNAKKE 888

Qy         58 YIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEA 117
              |:|:|: :  |  ||||| :: |: :|       |  |    || :|: :  |: |  :
Db        889 YMGLAIKNDNLVYVYNLGMKDVEILLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVPS 946

Qy        118 TSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDL 177
              |:  :   :  |    ::||:| ||| |||||| | :|:||: |  | | ||::||  |
Db        947 LSSTAEEKFIKKGEFAGDDSLLDLTPEDTVFYVGGVPANFKLPASLNLPSYSGCLELATL 1006

Qy        178 NENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYA--RIPTQPN--AP 228
              | :|:|||||  :|:: ::  || | |       :   :|:|: ||  |  |:
Db       1007 NNDVISLYNFKHIYNMDPSKSVPCARDKLAFTQSRAASYFFDGSSYAVVRDITRRGKFGQ 1066

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLN-SEPPKEKGIRDT---- 283
                |  |:|  | ||:    |  | || : :| | | |    |  |    : ||
Db       1067 VTRFDIEIRTPADNGLVLLMVNGSMFFSLEMRNGYLHVFYDFGFSNGPVH--LEDTLKKA 1124

Qy        284 -INDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIPIAIRERFNI 339
               ||| | | | | |    |:| : |: | |:    | :   |:  |:|| |  :  :
Db       1125 QINDAKYHEISI-IYHNDKKMILVVDRRHVKSTDNEKKKIPFTDIYIGGAPQEVLQSRTL 1183

Qy        340 STPA-----FQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFT 391
                  |:||||     ||   ::   :|:||   | ||  : | | |:  ||
Db       1184 RAHLPLDINFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIA 1241

Qy        392 NLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSP 450
              ::  :   | |:  | |:| ||:|  |  : : :    ::|::| : :  :   | :  :
Db       1242 SIQKISFFDGFEGGFNFRTLQPNGLLFYYTSGSDVFSISLDNGTVVMDVK--GIKVMSTD 1299

Qy        451 GTYMDGLLHH-VSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQQS------LRLGG---- 499
```

```
Db       1300 KQYHDGLPHFVVTSISDTR-YELVVDKSRLRGKN--PTKGKAEQTQTTEKKFYFGGSPIS 1356

Qy        500 ---GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 556

Db       1357 PQYANFTGCISNAYFTRLDRDVEVEDFQRYSEKVHTSLYECPIESSPLFLLHKKGKNSSK 1416


RESULT 15
Q6ZQA1
ID   Q6ZQA1      PRELIMINARY;      PRT;  1524 AA.
AC   Q6ZQA1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MKIAA0533 protein (Fragment).
GN   Name=mKIAA0533;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryonic tail;
RX   PubMed=14621295;
RA   Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA   Saga Y., Nagase T., Ohara O., Koga H.;
RT   "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT   III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT   cDNAs identified by screening of terminal sequences of cDNA clones
RT   randomly sampled from size-fractionated libraries.";
RL   DNA Res. 10:167-180(2003).
DR   EMBL; AK129157; BAC97967.2; -.
DR   GO; GO:0005604; C:basement membrane; IDA.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005178; F:integrin binding; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0001763; P:branching morphogenesis; IDA.
DR   GO; GO:0030324; P:lung development; IMP.
DR   GO; GO:0007517; P:muscle development; IMP.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR001368; TNFR_c6.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00053; Laminin_EGF; 2.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   SMART; SM00180; EGF_Lam; 2.
DR   SMART; SM00282; LamG; 5.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_3.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
KW   Laminin EGF-like domain.
FT   NON_TER      1      1
FT   NON_TER    1524   1524
SQ   SEQUENCE   1524 AA;  166516 MW;  F43411828FF8E691 CRC64;

  Query Match           23.2%;  Score 683;  DB 2;  Length 1524;
  Best Local Similarity   31.8%;  Pred. No. 1.8e-37;
  Matches  186;  Conservative  111;  Mismatches  210;  Indels   78;  Gaps   22;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGG--TEDMFVMYLGNKDASKDY 58

Db        572 MKFNGRSGVRLRTPRDLADLAAYTALKFHIQSPVPAPEPGKNTGDHFVLYMGSRQATGDY 631

Qy         59 IGMAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEA 117

Db        632 MGVSLRNQKVHWVYRLGKAGPTTLSIDENIGEQ------FAAVSIDRTLQFGHMSVTVE- 684

Qy        118 TSNKPKAPAVYDLEGGS----SNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIE 173

Db        685 ------KQMVHEIKGDTVAPGSEGLLNLHPDDFVFYVGGYPSNFTPPEPLRFPGYLGCIE 738

Qy        174 LDDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPNAP 228

Db        739 METLNEEVVSLYNFEQTFMLDTAVDKPCARSKATGDPWLTDGSYLDGSGFARISFEKQ-- 796

Qy        229 FPN---FIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPPK- 276

Db        797 FSNTKRFDQELRLVSYNGIIFFLKQESQFLCLAVQEGTLVLFYDFGSGLKKADPLQPPQA 856

Qy        277 ----EKGIRDTINDGKDHSILITIGKLQKRMWINVNERSVRIEGEIFDFSTYYLGGI--- 329

Db        857 LTAASKAIQVFLLAGNRKRVLV---RVERATVFSVDQDNML---EMAD--AYYLGGVPPE 908

Qy        330 --PIAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSR 384

Db        909 QLPLSLRQLFP-SGGSVRGCIKGIKALGKYVDLKRLN-TTGISFGCTADLLVGRTMTFHG 966

Qy        385 GGQMSFTNLDV-PSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSN 443

Db        967 HGFLPLALPDVAPITEVVYSGFGFRGTQDNNLLYYRTSPDGPYQVSLREGHVTLRFMNQE 1026

Qy        444 IPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDD--QVLRRNQRLPSFSNAQ----QSLRL 497

Db       1027 V---ETQRVFADGAPHYVAFYSNVTGVWLYVDDQLQLVKSHERTTPMLQLQPEEPSRLLL 1083

Qy        498 GG-------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLG 535

Db       1084 GGLPVSGTFHNFSGCISNVFVQRLRGPQRVFDLHQNMGSVNVSVG 1128


Search completed: February 22, 2005, 08:24:23
Job time : 98.5943 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:04:10 ; Search time 104.16 Seconds
(without alignments)
2097.921 Million cell updates/sec

Title: US-10-817-423-4
Perfect score: 2940
Sequence: 1 MRFNGKSGVEVRLPNDLEDL.....MLFKSPKRFNKGRIFNVNQL 565

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2940	100.0	1694	3	AAB48461	Aab48461 Rat lamin
2	2940	100.0	1725	3	AAB48460	Aab48460 Rat lamin
3	2439	83.0	1693	3	AAB48459	Aab48459 Human lam
4	2439	83.0	1693	3	AAB48457	Aab48457 Human lam
5	2439	83.0	1713	3	AAB48458	Aab48458 Human lam
6	2439	83.0	1713	6	ABR92102	Abr92102 Human cer
7	2439	83.0	1713	7	ADD29904	Add29904 Human lam
8	2439	83.0	1713	7	ADG37225	Adg37225 Human lam
9	2439	83.0	1713	8	ABM81957	Abm81957 Tumour-as
10	2439	83.0	1713	8	ADR87606	Adr87606 Human Lam
11	2439	83.0	1724	3	AAB48456	Aab48456 Human lam
12	2439	83.0	3332	7	ADE08094	Ade08094 Novel pro
13	2431	82.7	1713	2	AAR70148	Aar70148 Deduced s
14	1310	44.6	770	2	AAW26584	Aaw26584 Rat hemid
15	717.5	24.4	3597	5	ABB09503	Abb09503 Human lam
16	717.5	24.4	3600	5	ABB09501	Abb09501 Human lam
17	717	24.4	3690	8	ADM87254	Adm87254 Human pro
18	715	24.3	1677	8	ADM87708	Adm87708 Human EST
19	715	24.3	3695	5	ADI28030	Adi28030 ECMCAD pr
20	715	24.3	3695	8	ADN04478	Adn04478 Antipsori
21	715	24.3	3696	5	AAE17310	Aae17310 Human lam
22	715	24.3	3705	5	AAE17309	Aae17309 Human lam
23	712	24.2	1601	4	AAM39009	Aam39009 Human pol
24	712	24.2	1640	5	ABB09504	Abb09504 Human lam
25	712	24.2	1640	8	ADO10049	Ado10049 Novel hum
26	712	24.2	1645	7	ADL15098	Adl15098 Human mal
27	712	24.2	1645	7	ADN95658	Adn95658 Human BEC
28	712	24.2	3695	5	ABB81588	Abb81588 Human lam
29	694	23.6	1792	3	AAB48443	Aab48443 Human lam
30	694	23.6	1800	3	AAB48445	Aab48445 Human lam
31	694	23.6	1816	3	AAB48442	Aab48442 Human lam
32	694	23.6	1816	8	ADR87600	Adr87600 Human Lam
33	694	23.6	1824	3	AAB48444	Aab48444 Human lam
34	688	23.4	1823	5	ABP63020	Abp63020 Human pol
35	686.5	23.4	3597	8	ADO10047	Ado10047 Novel hum
36	686	23.3	1581	7	ADJ68348	Adj68348 Human hea
37	686	23.3	1816	8	ADP08401	Adp08401 Human lam
38	685	23.3	953	5	AAM50358	Aam50358 Human lam
39	683	23.2	984	5	ABB80819	Abb80819 Heparin b
40	683	23.2	1792	3	AAB48447	Aab48447 Mouse lam
41	683	23.2	1816	3	AAB48446	Aab48446 Mouse lam
42	683	23.2	1816	7	ADC01877	Adc01877 Human lam
43	681	23.2	1816	7	ADC01879	Adc01879 Human lam
44	681	23.2	3635	5	ABB81589	Abb81589 Mouse lam
45	681	23.2	3635	5	AAM50357	Aam50357 Mouse lam

ALIGNMENTS

RESULT 1
AAB48461
ID AAB48461 standard; protein; 1694 AA.
XX
AC AAB48461;
XX
DT 02-MAR-2001 (first entry)
XX
DE Rat laminin 5 polypeptide, SEQ ID NO: 12.
XX
KW Rat; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS Rattus norvegicus.
XX
PN WO200066731-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011459.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (BIOS-) BIOSTATUM INC.
XX
PI Boutaud A;
XX
DR WPI; 2000-687538/67.
DR N-PSDB; AAC83722.
XX
PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burns, acute wounds and skin grafts.
XX
PS Claim 3; Page 117-122; 232pp; English.
XX
CC The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of Type
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotrimeric laminin, whereas

```
CC   prior art cell lines have been created that produce but do not secreted
CC   only one or two chain laminins
XX
SQ   Sequence 1694 AA;

  Query Match             100.0%;  Score 2940;  DB 3;  Length 1694;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-261;
  Matches  565;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 810

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 870

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 930

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 990

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 1050

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 1110

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 1170

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 1230

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 1290

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              |||||||||||||||||||||||||
Db       1291 KPPFLMLFKSPKRFNKGRIFNVNQL 1315


RESULT 2
AAB48460
ID   AAB48460 standard; protein; 1725 AA.
XX
AC   AAB48460;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Rat laminin 5 polypeptide, SEQ ID NO: 10.
XX
KW   Rat; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW   cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW   periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS   Rattus norvegicus.
XX
PN   WO200066731-A2.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011459.
XX
PR   30-APR-1999;   99US-0131720P.
PR   21-AUG-1999;   99US-0149738P.
PR   24-SEP-1999;   99US-0155945P.
XX
PA   (BIOS-) BIOSTATUM INC.
XX
PI   Boutaud A;
XX
DR   WPI; 2000-687538/67.
DR   N-PSDB; AAC83721.
XX
PT   Laminin 5-expressing cells, used to accelerate wound healing associated
PT   with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT   burns, acute wounds and skin grafts.
XX
PS   Claim 3; Page 104-109; 232pp; English.
XX
CC   The present sequence is a laminin 5 chain polypeptide. Recombinant
CC   laminin 5-expressing cells are used to accelerate wound healing,
CC   especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC   surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC   intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC   improve the biocompatibility of medical devices, and to promote cell
CC   adhesion to a surface. They can be used for the ex vivo treatment of Type
CC   I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC   line produces and secretes recombinant heterotrimeric laminin, whereas
CC   prior art cell lines have been created that produce but do not secreted
CC   only one or two chain laminins
XX
SQ   Sequence 1725 AA;

  Query Match             100.0%;  Score 2940;  DB 3;  Length 1725;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-261;
  Matches  565;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 841

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 901

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 961

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 1021

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 1081

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 1141

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 1201

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 1261

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 1321

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              |||||||||||||||||||||||||
Db       1322 KPPFLMLFKSPKRFNKGRIFNVNQL 1346
```

```
RESULT 3
AAB48459
ID   AAB48459 standard; protein; 1693 AA.
XX
AC   AAB48459;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human laminin 5 polypeptide, SEQ ID NO: 8.
XX
KW   Human; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW   cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW   periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS   Homo sapiens.
XX
PN   WO200066731-A2.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011459.
XX
PR   30-APR-1999;   99US-0131720P.
PR   21-AUG-1999;   99US-0149738P.
PR   24-SEP-1999;   99US-0155945P.
XX
PA   (BIOS-) BIOSTATUM INC.
XX
PI   Boutaud A;
XX
DR   WPI; 2000-687538/67.
DR   N-PSDB; AAC83720.
XX
PT   Laminin 5-expressing cells, used to accelerate wound healing associated
PT   with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT   burns, acute wounds and skin grafts.
XX
PS   Claim 3; Page 91-97; 232pp; English.
XX
CC   The present sequence is a laminin 5 chain polypeptide. Recombinant
CC   laminin 5-expressing cells are used to accelerate wound healing,
CC   especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC   surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC   intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC   improve the biocompatibility of medical devices, and to promote cell
CC   adhesion to a surface. They can be used for the ex vivo treatment of Type
CC   I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC   line produces and secretes recombinant heterotrimeric laminin, whereas
CC   prior art cell lines have been created that produce but do not secreted
CC   only one or two chain laminins
XX
SQ   Sequence 1693 AA;

  Query Match             83.0%;  Score 2439;  DB 3;  Length 1693;
  Best Local Similarity   81.9%;  Pred. No. 3e-215;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        751 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 810

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::||||||||||||||:||||| |||:
Db        811 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 870

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:|||||  ||||||||||||||||
Db        871 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 930

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| |||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        931 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 990

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db        991 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1050

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||||:|||||||||||||||
Db       1051 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1110

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1111 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1170

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1171 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1230

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ::||   |:::|||||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1231 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1290

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1291 KPPFLMLLKGSTRFNKTKTFRINQL 1315


RESULT 4
AAB48457
ID   AAB48457 standard; protein; 1693 AA.
XX
AC   AAB48457;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human laminin 5 polypeptide, SEQ ID NO: 4.
XX
KW   Human; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW   cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW   periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS   Homo sapiens.
XX
PN   WO200066731-A2.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011459.
XX
PR   30-APR-1999;   99US-0131720P.
PR   21-AUG-1999;   99US-0149738P.
PR   24-SEP-1999;   99US-0155945P.
XX
PA   (BIOS-) BIOSTATUM INC.
XX
PI   Boutaud A;
XX
DR   WPI; 2000-687538/67.
DR   N-PSDB; AAC83718.
XX
PT   Laminin 5-expressing cells, used to accelerate wound healing associated
PT   with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT   burns, acute wounds and skin grafts.
XX
PS   Claim 3; Page 66-71; 232pp; English.
XX
CC   The present sequence is a laminin 5 chain polypeptide. Recombinant
CC   laminin 5-expressing cells are used to accelerate wound healing,
CC   especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC   surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC   intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC   improve the biocompatibility of medical devices, and to promote cell
CC   adhesion to a surface. They can be used for the ex vivo treatment of Type
```

```
CC   I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC   line produces and secretes recombinant heterotrimeric laminin, whereas
CC   prior art cell lines have been created that produce but do not secreted
CC   only one or two chain laminins
XX
SQ   Sequence 1693 AA;

  Query Match             83.0%;  Score 2439;  DB 3;  Length 1693;
  Best Local Similarity   81.9%;  Pred. No. 3e-215;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        751 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 810

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        811 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 870

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db        871 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 930

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| |||||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        931 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 990

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db        991 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1050

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||||:|||||||||||||||
Db       1051 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1110

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1111 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1170

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1171 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1230

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::||||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1231 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1290

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1291 KPPFLMLLKGSTRFNKTKTFRINQL 1315


RESULT 5
AAB48458
ID   AAB48458 standard; protein; 1713 AA.
XX
AC   AAB48458;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human laminin 5 polypeptide, SEQ ID NO: 6.
XX
KW   Human; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW   cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW   periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS   Homo sapiens.
XX
PN   WO200066731-A2.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011459.
XX
PR   30-APR-1999;   99US-0131720P.
PR   21-AUG-1999;   99US-0149738P.
PR   24-SEP-1999;   99US-0155945P.
XX
PA   (BIOS-) BIOSTATUM INC.
XX
PI   Boutaud A;
XX
DR   WPI; 2000-687538/67.
DR   N-PSDB; AAC83719.
XX
PT   Laminin 5-expressing cells, used to accelerate wound healing associated
PT   with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT   burns, acute wounds and skin grafts.
XX
PS   Claim 3; Page 79-84; 232pp; English.
XX
CC   The present sequence is a laminin 5 chain polypeptide. Recombinant
CC   laminin 5-expressing cells are used to accelerate wound healing,
CC   especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC   surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC   intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC   improve the biocompatibility of medical devices, and to promote cell
CC   adhesion to a surface. They can be used for the ex vivo treatment of Type
CC   I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC   line produces and secretes recombinant heterotrimeric laminin, whereas
CC   prior art cell lines have been created that produce but do not secreted
CC   only one or two chain laminins
XX
SQ   Sequence 1713 AA;

  Query Match             83.0%;  Score 2439;  DB 3;  Length 1713;
  Best Local Similarity   81.9%;  Pred. No. 3.1e-215;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| |||||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||||:|||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::||||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
```

```
                ||||||| |    |||| : | :|||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 6
ABR92102
ID   ABR92102 standard; protein; 1713 AA.
XX
AC   ABR92102;
XX
DT   10-SEP-2003  (first entry)
XX
DE   Human cervical cancer cell marker encoding cDNA SEQ ID NO:113.
XX
KW   Human; cervical cancer; cervical cancer marker; cancer therapy;
KW   detection; gene therapy; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO2002101075-A2.
XX
PD   19-DEC-2002.
XX
PF   12-JUN-2002; 2002WO-US018638.
XX
PR   13-JUN-2001; 2001US-0298155P.
PR   13-JUN-2001; 2001US-0298159P.
PR   14-NOV-2001; 2001US-0335936P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Schlegel R, Chen Y, Zhao X, Monahan JE, Kamatkar S;
PI   Gannavarapu M, Glatt K, Hoersch S;
XX
DR   WPI; 2003-156967/15.
DR   N-PSDB; ACF12884.
XX
PT   New isolated nucleic acid molecule useful for detecting, characterizing,
PT   preventing and treating human cervical cancers, in various prognostic and
PT   diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
XX
PS   Claim 4; Page 269-273; 386pp; English.
XX
CC   ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)
CC   given in ABR92047 to ABR92164. A higher level of expression of (I) than
CC   normal indicates the presence of cervical cancer. Also described: (1) a
CC   vector (II) containing (I); (2) a host cell (III) containing (I); and (3)
CC   assessing (M1) whether a patient is afflicted with cervical cancer,
CC   comprising comparing the level of expression of a marker in a patient's
CC   sample, and the normal level of expression of the marker in a control non
CC   -cervical cancer sample, where a significant increase in the level of
CC   expression of the marker in the patient's sample relative to that in the
CC   control sample is an indication that the patient is afflicted with
CC   cervical cancer. (I) has cytostatic activity, and can be used in gene
CC   therapy and in vaccines. (I) is useful in detecting, characterising,
CC   preventing and treating human cervical cancers. (I) may also be used in
CC   various prognostic and diagnostic assays, pharmacogenomics and in
CC   monitoring clinical trials
XX
SQ   Sequence 1713 AA;

  Query Match             83.0%;  Score 2439;  DB 6;  Length 1713;
  Best Local Similarity   81.9%;  Pred. No. 3.1e-215;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||: |||||||:|||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:|||||  |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||||: |||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||:|||||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |    |||| : | :|||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 7
ADD29904
ID   ADD29904 standard; protein; 1713 AA.
XX
AC   ADD29904;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human laminin alpha 3 seq id 2.
XX
KW   ophthalmological; dermatological; laminin alpha 3; G3 domain;
KW   cell adhesion function; cell movement effect; epithelial tissue function;
KW   retinal detachment; cosmetic surgery; skin graft; human.
XX
OS   Homo sapiens.
XX
PN   JP2003093064-A.
XX
PD   02-APR-2003.
XX
PF   20-SEP-2001; 2001JP-00287519.
XX
PR   20-SEP-2001; 2001JP-00287519.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA   (KIHA-) ZH KIHARA KINEN YOKOHAMA SEIMEI KAGAKU.
XX
DR   WPI; 2003-817304/77.
DR   N-PSDB; ADD29903.
XX
PT   Novel modified G3 domain of laminin alpha 3 chain useful for controlling
PT   cell adhesion and cell movement.
XX
PS   Claim 1; SEQ ID NO 2; 49pp; Japanese.
XX
CC   The invention describes a modified laminin alpha3 chain comprising one or
CC   more amino acid deletions, substitutions or additions at region
CC   corresponding to a region of G3 domain having amino acids 1214-1324 of
CC   laminin alpha3 chain having a fully defined sequence of 1713 amino acids
CC   as given in the specification. (I) can control cell adhesion function and
```

```
CC   cell movement effect. A composition comprising laminin is useful for
CC   maintaining or treating the function of epithelial tissue and for
CC   treatment or prevention of retinal detachment and in cosmetic surgery and
CC   skin graft. The modified region of laminin alpha3 chain can control cell
CC   adhesion function and cell movement effect. This is the amino acid
CC   sequence of human laminin alpha 3.
XX
SQ   Sequence 1713 AA;

  Query Match             83.0%;  Score 2439;  DB 7;  Length 1713;
  Best Local Similarity   81.9%;  Pred. No. 3.1e-215;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||: |||||||:|||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:::|||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :||||||||||: ||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||||:|||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::||||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 8
ADG37225
ID   ADG37225 standard; protein; 1713 AA.
XX
AC   ADG37225;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human laminin-6 alpha 3 subunit.
XX
KW   human; laminin-6; alpha 3; B1 subunit; B2 subunit; cell-movement;
KW   cell-adhesion; dermatological; neuroprotective; muscular;
KW   epithelial tissue; nervous tissue; varicella disease.
XX
OS   Homo sapiens.
XX
PN   JP2003212791-A.
XX
PD   30-JUL-2003.
XX
PF   17-JAN-2002; 2002JP-00009227.
XX
PR   17-JAN-2002; 2002JP-00009227.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2003-819867/77.
DR   N-PSDB; ADG37224.
XX
PT   Composition comprising laminin-6 for regulation of cell-movement activity
PT   and/or cell-adhesion activity, useful for treating or maintaining
PT   function of epithelial tissue, nervous tissue and muscles.
XX
PS   Claim 2; SEQ ID NO 2; 55pp; Japanese.
XX
CC   This invention describes a novel composition comprising the human laminin
CC   -6 alpha 3, B1 or B2 subunits for regulation of cell-movement activity
CC   and/or cell-adhesion activity. The products of the invention have
CC   dermatological, neuroprotective and muscular activity. The composition of
CC   the invention is useful for treating or maintaining the function of the
CC   epithelial tissue, the nervous tissue and muscles and is also useful for
CC   treatment or prevention of varicella disease.
XX
SQ   Sequence 1713 AA;

  Query Match             83.0%;  Score 2439;  DB 7;  Length 1713;
  Best Local Similarity   81.9%;  Pred. No. 3.1e-215;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||: |||||||:|||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:::|||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :||||||||||: ||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||||:|||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::||||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 9
ABM81957
```

```
ID   ABM81957 standard; protein; 1713 AA.
XX
AC   ABM81957;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Tumour-associated antigenic target (TAT) polypeptide PRO2799, SEQ:5041.
XX
KW   Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW   tumour; diagnosis; cell proliferative disorder; breast cancer;
KW   colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW   central nervous system cancer; bladder cancer; pancreatic cancer;
KW   cervical cancer; melanoma; leukaemia; hybridisation probe;
KW   chromosome identification; chromosome mapping; gene mapping;
KW   gene therapy; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2004030615-A2.
XX
PD   15-APR-2004.
XX
PF   29-SEP-2003; 2003WO-US028547.
XX
PR   02-OCT-2002; 2002US-0414971P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Wu TD,  Zhang Z,  Zhou Y;
XX
DR   WPI; 2004-347921/32.
DR   N-PSDB; ACN40327.
XX
PT   New tumor-associated antigenic target polypeptides and nucleic acids,
PT   useful in preparing a medicament for treating or detecting a
PT   proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT   prostate cancer or tumor.
XX
PS   Claim 12; SEQ ID NO 5041; 7273pp; English.
XX
CC   The invention relates to human tumour-associated antigenic target (TAT)
CC   polypeptides, and their related nucleic acids. The TAT polypeptides are
CC   overexpressed in cancer tissues compared to normal tissues, and may thus
CC   serve as effective targets for the diagnosis and treatment of cancer in
CC   mammals. The invention also relates to nucleic acid and polypeptide
CC   sequences at least 80% identical to the TAT nucleic acids and
CC   polypeptides; expression vectors and host cells comprising a TAT nucleic
CC   acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC   molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC   TAT polypeptide; and methods and compositions for the treatment or
CC   diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC   antibodies, antagonists, binding molecules and compositions are useful
CC   for diagnosing or treating a cell proliferative disorder associated with
CC   increased TAT expression, particularly cancers such as breast cancer,
CC   colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC   cancer, pancreatic cancer, cervical cancer, cancers of the central
CC   nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC   used as hybridisation probes, in chromosome and gene mapping, in
CC   chromosome identification and in gene therapy. The present sequence
CC   represents a TAT polypeptide of the invention
XX
SQ   Sequence 1713 AA;

  Query Match             83.0%;  Score 2439;  DB 8;  Length 1713;
  Best Local Similarity   81.9%;  Pred. No. 3.1e-215;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :||||||||||: ||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||||:|||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||   | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 10
ADR87606
ID   ADR87606 standard; protein; 1713 AA.
XX
AC   ADR87606;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Human Laminin alpha 3 (nicein), SEQ ID 10.
XX
KW   Cytostatic; Gene Therapy; renal cell carcinoma; Wilms tumour; human;
KW   Laminin alpha 3; nicein.
XX
OS   Homo sapiens.
XX
PN   WO2004075835-A2.
XX
PD   10-SEP-2004.
XX
PF   20-FEB-2004; 2004WO-US005042.
XX
PR   21-FEB-2003; 2003US-00372683.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Gerritsen ME,  Peale FV,  Wu TD;
XX
DR   WPI; 2004-676901/66.
DR   N-PSDB; ADR87605.
XX
PT   New anti-EDNRA antibody, useful in preparing a composition for diagnosing
PT   or inhibiting the growth of renal cell carcinoma or Wilms tumor.
XX
PS   Example 1; SEQ ID NO 10; 257pp; English.
XX
CC   The present invention relates to novel antibodies which bind to proteins
CC   which are overexpressed in renal cell carcinomas or Wilms tumour. The
CC   antibody can bind to a protein comprising CXCR4 (ADR87598), Laminin alpha
```

```
CC   4 (ADR87600), TIMP1 (ADR87602), Type IV collagen alpha 1 (ADR87604),
CC   Laminin alpha 3 (nicein) (ADR87606), Adrenomedullin (ADR87608), Type IV
CC   collagen alpha 2 (ADR87610), Thrombospondin 2 (ADR87612), Type I collagen
CC   alpha 2 (ADR87614), Type VI collagen alpha 3 (ADR87616), Latent TGFbeta
CC   binding protein 2 (LTBP2) (ADR87618), Serine or cystein protease
CC   inhibitor heat shock protein 47 (HSP47) (ADR87620), Procollagen-lysine, 2
CC   -oxoglutarate 5-dioxygenase (ADR87622), connexin 43 (ADR87624), Type IV
CC   collagen alpha 2 (ADR87626), Connexin 37 (ADR87628), Ephrin A1
CC   (ADR87630), Laminin beta 2 (ADR87632), Integrin alpha 1, hevin
CC   (ADR87635), Stanniocalcin 1 (ADR87637), Thrombospondin 4 (ADR87639), CD36
CC   polypeptide (ADR87641), Endothelin receptor A (EDNRA, ADR87643) or
CC   Endothelin receptor B (EDNRB ADR87645). The proteins of ADR87598-ADR87641
CC   and ADR87645 are all overexpressed in renal call carcinoma, and ADR87643
CC   (EDNRA) is overexpressed in Wilms tumour. The antibodies are useful in
CC   preparing a composition for diagnosing or inhibiting the growth of renal
CC   cell carcinoma or Wilms tumour. The present sequence is one such protein
CC   of the invention.
XX
SQ   Sequence 1713 AA;

  Query Match            83.0%;  Score 2439;  DB 8;  Length 1713;
  Best Local Similarity  81.9%;  Pred. No. 3.1e-215;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: |||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||:|||||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:|: :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:||||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| |||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 11
AAB48456
ID   AAB48456 standard; protein; 1724 AA.
XX
AC   AAB48456;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human laminin 5 polypeptide, SEQ ID NO: 2.
XX
KW   Human; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW   cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW   periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS   Homo sapiens.
XX
PN   WO200066731-A2.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011459.
XX
PR   30-APR-1999;   99US-0131720P.
PR   21-AUG-1999;   99US-0149738P.
PR   24-SEP-1999;   99US-0155945P.
XX
PA   (BIOS-) BIOSTATUM INC.
XX
PI   Boutaud A;
XX
DR   WPI; 2000-687538/67.
DR   N-PSDB; AAC83717.
XX
PT   Laminin 5-expressing cells, used to accelerate wound healing associated
PT   with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT   burns, acute wounds and skin grafts.
XX
PS   Claim 3; Page 53-59; 232pp; English.
XX
CC   The present sequence is a laminin 5 chain polypeptide. Recombinant
CC   laminin 5-expressing cells are used to accelerate wound healing,
CC   especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC   surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC   intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC   improve the biocompatibility of medical devices, and to promote cell
CC   adhesion to a surface. They can be used for the ex vivo treatment of Type
CC   I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC   line produces and secretes recombinant heterotrimeric laminin, whereas
CC   prior art cell lines have been created that produce but do not secreted
CC   only one or two chain laminins
XX
SQ   Sequence 1724 AA;

  Query Match            83.0%;  Score 2439;  DB 3;  Length 1724;
  Best Local Similarity  81.9%;  Pred. No. 3.1e-215;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        782 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 841

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::||||||||||||||:||||| |||:
Db        842 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 901

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: |||||||||||:||||| ||||||||||||||||
Db        902 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 961

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        962 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1021

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||| |||:|: | ||:|:|||| | |||||
Db       1022 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1081

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||:|||||||||||||||||
Db       1082 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1141
```

```
Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1142 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1201

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1202 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1261

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1262 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1321

Qy        541 KPPPLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1322 KPPFLMLLKGSTRFNKTKTFRINQL 1346
```

RESULT 12
ADE08094
ID ADE08094 standard; protein; 3332 AA.
XX
AC ADE08094;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel protein (useful for identifying genetic disorders) #249.
XX
KW novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder.
XX
OS Unidentified.
XX
PN WO2003054152-A2.
XX
PD 03-JUL-2003.
XX
PF 10-DEC-2002; 2002WO-US039555.
XX
PR 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.
PR 12-APR-2002; 2002US-0372381P.
PR 12-APR-2002; 2002US-0372615P.
PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376045P.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
DR WPI; 2003-569235/53.
DR N-PSDB; ADE07183.
XX
PT New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.
XX
PS Claim 20; SEQ ID NO 1160; 1177pp; English.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present amino acid sequence represents a protein
CC of the invention.
XX
SQ Sequence 3332 AA;

```
  Query Match           83.0%;  Score 2439;  DB 7;  Length 3332;
  Best Local Similarity  81.9%;  Pred. No. 8.9e-215;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||: |||||||:|||||||||||:||||
Db       2390 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 2449

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQPAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:|:||::|||||||||||||||:||||| |||:
Db       2450 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQPARLNYTKGATSS 2509

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db       2510 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 2569

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||:||||:|| | | |||||||
Db       2570 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 2629

Qy        241 DRGLLPFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       2630 DRGLLPFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 2689

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||:|||||||||||||||||
Db       2690 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 2749

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       2750 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 2809

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       2810 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 2869

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       2870 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 2929

Qy        541 KPPPLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       2930 KPPFLMLLKGSTRFNKTKTFRINQL 2954
```

RESULT 13
AAR70148
ID AAR70148 standard; protein; 1713 AA.
XX
AC AAR70148;
XX
DT 25-MAR-2003 (revised)
DT 05-OCT-1995 (first entry)
XX
DE Deduced sequence of cDNA corresp. to the alpha-3EpA transcript.
XX
KW E170; epithelial ligand glycoprotein; epiligrin complex;
KW epithelial cell binding.
XX
OS Homo sapiens.
XX
PN WO9506660-A1.
XX
PD 09-MAR-1995.
XX
PF 02-SEP-1994; 94WO-US010261.
XX
PR 02-SEP-1993; 93US-00115918.
XX
PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
XX
PI Carter WG, Gil SG, Ryan MC;
XX

```
DR   WPI; 1995-115398/15.
DR   N-PSDB; AAQ83236.
XX
PT   New nucleic acid encoding epiligrin, an epithelial ligand complex - also
PT   related vectors, transformed cells, proteins and antibodies, useful
PT   therapeutically and diagnostically, e.g., in cases of inflammation and to
PT   induce cancer cell differentiation.
XX
PS   Claim 12; Fig 15A-F; 187pp; English.
XX
CC   AAQ83235 depicts the nt. sequence compiled from sequencing cDNA clones
CC   corresp. to the alpha-3 EpA transcript. The invention includes nt
CC   sequences in the gp. comprising the nt sequence shown in AAQ83235, the
CC   cDNA clone Ep-1 (ATCC No. 75540) shown in AAQ83234, the cDNA clone 1-1
CC   (ATCC No. 75539), and the cDNA clone 8-6 (ATCC No. 75538), or the nt.
CC   sequences shown in AAQ83236. The entire nt region encoding E170 is
CC   depicted in AAQ83236, and corresp. to the SQ of alpha-3. AAQ83236
CC   consists of a composite sequence derived from several overlapping clones.
CC   A synthetic polypeptide of at least 5 AAs that corresp. to part or all of
CC   the nt. sequence shown in AAQ83236 is claimed. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 1713 AA;

  Query Match             82.7%;  Score 2431;  DB 2;  Length 1713;
  Best Local Similarity   81.8%;  Pred. No. 1.7e-214;
  Matches  462;  Conservative   47;  Mismatches   56;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||:|:||:||:||::||||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||| | ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSPLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIHIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||||:|||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | |||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 14
AAW26584
ID   AAW26584 standard; protein; 770 AA.
XX
AC   AAW26584;
XX
DT   25-MAR-2003  (revised)
DT   21-JAN-1998  (first entry)
XX
DE   Rat hemidesmosome formation inducing protein 154 kDa subunit.
XX
KW   Hemidesmosome; laminin; epithelial cell; cell attachment; adhesion;
KW   bladder carcinoma; 804G; NBT-II; rat; dental implant.
XX
OS   Rattus sp.
XX
PN   US5658789-A.
XX
PD   19-AUG-1997.
XX
PF   19-MAY-1995;   95US-00445135.
XX
PR   12-NOV-1993;   93US-00151134.
XX
PA   (DESM-) DESMOS INC.
XX
PI   Hormia M,  Quaranta V;
XX
DR   WPI; 1997-424242/39.
XX
PT   Soluble protein that induces hemi:desmosome formation in epithelial cells
PT   - useful for stimulating epithelial cell attachment, e.g. to dental
PT   implants or teeth.
XX
PS   Claim 2; Col 21-26; 20pp; English.
XX
CC   This polypeptide comprises the 154 kDa alpha chain of an isolated soluble
CC   protein that induces hemidesmosome formation in epithelial cells normally
CC   unable to form hemidesmosomes. The 146 kD gamma chain (see AAW26584) and
CC   the N-terminal portion (see AAW26585) of the 139 kDa beta chain sequence
CC   were also determined. The protein has properties including: (a)
CC   solubility in aqueous media; (b) binding by antibodies present in the
CC   serum of rabbits inoculated with an extracellular matrix deposited by
CC   804G rat bladder carcinoma cells or NBT-II rat bladder carcinoma cells;
CC   (c) being bound by monoclonal antibodies generated against extracellular
CC   matrix; (d) promoting rapid epithelial cell adhesion to substrates coated
CC   with at least one of the three protein chains; and (e) being obtainable
CC   from 804G rat bladder carcinoma cells or NBT-II rat bladder carcinoma
CC   cells. The protein (secreted laminin) is used to induce hemidesmosome
CC   formation in epithelial cells and to facilitate their growth (claimed).
CC   It may be used to promote cell attachment to solid surfaces, e.g. to
CC   dental implants, and may also be of use in studies concerning
CC   hemidesmosome morphogenesis and alpha 6 beta 4 integrin interactions with
CC   the epithelial extracellular matrix. (Updated on 25-MAR-2003 to correct
CC   PF field.)
XX
SQ   Sequence 770 AA;

  Query Match             44.6%;  Score 1310;  DB 2;  Length 770;
  Best Local Similarity   90.9%;  Pred. No. 2.1e-111;
  Matches  259;  Conservative    3;  Mismatches   13;  Indels   10;  Gaps    4;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 550

Qy         61 MA----VVDGQLTCVYNLGDREAEVQIDQV-LTESESQEAVMDRVKFQRIYQFAKLNYTK 115
              :    |    |:   | |   |  |:  |||||||||||||||||||||||||||||
Db        551 IGGCRWPAD---VCLQPGGPR--SVSSDRSGLTESESQEAVMDRVKFQRIYQFAKLNYTK 605

Qy        116 EATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELD 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 EATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELD 665

Qy        176 DLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQT 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 DLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQT 725
```

```
Qy        236 IQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGI 280
              ||||| |||||||||||||||||||||||||||||||||||||||
Db        726 IQTTVARGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGI 770


RESULT 15
ABB09503
ID   ABB09503 standard; protein; 3597 AA.
XX
AC   ABB09503;
XX
DT   01-NOV-2002  (first entry)
XX
DE   Human laminin alpha-5-like NOV1c protein, SEQ ID NO:6.
XX
KW   Human; NOVX; neurological disorder; Alzheimer's disease;
KW   Huntington's disease; Parkinson's disease; pain; behavioural disorder;
KW   addiction; tuberous sclerosis; cancer; immune disorder; allergy;
KW   autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;
KW   thyroiditis; cardiovascular disease; hypertension; reproductive disorder;
KW   endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;
KW   pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;
KW   polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;
KW   atherosclerosis; cell signal processing-related disorder;
KW   metabolic pathway regulation disorder; cytostatic; neuroprotective;
KW   antiinflammatory; immunosuppressive; analgesic; antiatherosclerotic;
KW   dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis;
KW   differentiation; proliferation; motility; haematopoiesis; wound healing;
KW   angiogenesis; forensic biology; transgenic animal; drug screening;
KW   gene therapy; NOV1c; laminin alpha-5-like; chromosome 20.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .14
FT                   /label= Signal_peptide
FT   Protein         15. .3597
FT                   /note= "Mature NOV1c protein"
XX
PN   WO200253742-A2.
XX
PD   11-JUL-2002.
XX
PF   07-JAN-2002; 2002WO-US000375.
XX
PR   05-JAN-2001; 2001US-0260018P.
PR   08-JAN-2001; 2001US-0260360P.
PR   28-FEB-2001; 2001US-0272411P.
PR   02-MAR-2001; 2001US-0272817P.
PR   05-JUL-2001; 2001US-0303231P.
PR   12-JUL-2001; 2001US-0305060P.
PR   10-SEP-2001; 2001US-0318405P.
PR   12-SEP-2001; 2001US-0318700P.
PR   04-JAN-2002; 2002US-00037417.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Kekuda R,  Alsobrook JP,  Tchernev VT,  Liu X,  Spytek KA;
PI   Patturajan M,  Grosse WM,  Lepley DM,  Burgess CE,  Vernet CAM,  Li L;
PI   Gorman L,  Edinger S,  Sciore P,  Ellerman K,  Malyankar U;
PI   Rothenberg M,  Stone D,  Boldog F,  Guo X,  Shenoy S,  Anderson D;
PI   Padigaru M,  Taupier RJ,  Miller CE,  Eisen A;
XX
DR   WPI; 2002-583619/62.
DR   N-PSDB; ABQ93881.
XX
PT   Novel polypeptides and nucleic acids homologous to transmembrane
PT   receptor, thymosin, neuromodulin-like family of proteins for diagnosing,
PT   treating cancer, atherosclerosis, neurological, skin and autoimmune
PT   disorders.
XX
PS   Claim 1c; Page 20-21; 323pp; English.
XX
CC   The invention relates to 24 novel human proteins designated NOV1-NOV14
CC   (ABB09501-ABB09524), collectively referred to as NOVX proteins, and
CC   nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins and
CC   nucleotides are useful in the treatment, diagnosis or prevention of NOVX-
CC   associated disorders or in the manufacture of a medicament for treating
CC   such disorders, with specific applications described for each of the 24
CC   NOVX proteins, based on their homology to known proteins. Various
CC   disorders are associated with NOVX proteins including neurological
CC   disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),
CC   pain, behavioural disorders, addiction, tuberous sclerosis, cancers
CC   (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders
CC   (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma,
CC   various forms of arthritis, diabetes, thyroiditis, cardiovascular disease
CC   (e.g., hypertension), reproductive disorders, endometriosis,
CC   incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,
CC   cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocrine
CC   disorders, obesity, bacterial infections and particularly cardiomyopathy,
CC   atherosclerosis, cell signal processing-related disorders and disorders
CC   of metabolic pathway regulation. NOVX nucleic acids and polypeptides may
CC   be used to identify cellular receptors or downstream effectors which
CC   binds to a NOVX protein, and are also useful as targets for the
CC   identification of small molecules that modulate or inhibit processes such
CC   as neurogenesis, cell differentiation, cell motility, cellular
CC   proliferation, haematopoiesis, wound healing and angiogenesis. NOVX
CC   nucleic acid sequences can be used to identify a cell or tissue type and
CC   are useful as a source of primers or probes for forensic biology and for
CC   identifying and cloning NOVX homologues in other cell types. Cells
CC   comprising NOVX nucleic acids are useful for producing non-human
CC   transgenic animals which are useful for studying the function and
CC   activity of NOVX proteins and for identifying and evaluating modulators
CC   of NOVX activity. The present sequence represents the laminin alpha-5-
CC   like protein NOV1c. The gene encoding NOV1c is located on chromosome 20
XX
SQ   Sequence 3597 AA;

  Query Match           24.4%;  Score 717.5;  DB 5;  Length 3597;
  Best Local Similarity   31.7%;  Pred. No. 1.4e-55;
  Matches  200;  Conservative  100;  Mismatches  222;  Indels  109;  Gaps   22;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |:|||:|||::| | || ||  ||:|  :|| |:      |||| ||||:|:: |: ||:|
Db       2712 MKFNGRSGVQLRTPRDLADLAAYTALKFYLQGPEPEPGQGTEDRFVMYMGSRQATGDYMG 2771

Qy         61 MAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE--- 116
              ::: | ::  || ||:   | : ||: : |          |   |  ||  :: | |
Db       2772 VSLRDKKVHWVYQLGEAGPAVLSIDEDIGEQ------FAAVSLDRTLQFGHMSVTVERQM 2825

Qy        117 --ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIEL 174
                |      ||     ||     |||| |:| |||||||  |  |  |||| |:||||:
Db       2826 IQETKGDTVAPGA---EG-----LLNLRPDDFVFYVGGYPSTFTPPPLLRFPGYRGCIEM 2877

Qy        175 DDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPN-AP 228
              | ||| |:|||||: || |:|    || | |       :| :| :|||:|||      :
Db       2878 DTLNEEVVSLYNFERTFQLDTAVDRPCARSKSTGDPWLTDGSYLDGTGFARISFDSQIST 2937

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPP----- 275
                | | ::     |:||| : |  |: | :::|:|:: |   :         :||
Db       2938 TKRFEQELRLVSYSGVLFFLKQQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPPLTS 2997

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNER---SVRIEGEIFDFSTYYLGGIP-- 330
                | |:          :  :|  :||: : |      ||  : ::     |||||:|
Db       2998 ASKAIQ-----------VFLLGGSRKRVLVRVERATVYSVEQDNDLELADAYYLGGVPPD 3046

Qy        331 -IAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGG 386
               :    |   :  : :||:| :|   |   : ||| | ||:  |: | :  :|   |
Db       3047 QLPSLRRLFPTGGSVRGCVKGIKALGKYVDLKRLN-TTGVSAGCTADLLVGRAMTFHGHG 3105

Qy        387 --QMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNI 444
                ::: :|:  | |       ||| : | |  |     :       |:|: | : |    : :
Db       3106 FLRLALSNV-APLTGNVYSGFGFHSAQDSALLYYRASPVRPHQVSLQQGRVSLQLLRTEV 3164

Qy        445 PIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQV--LRRNQRLPSFSNAQQS----LRLG 498
```

```
                |:   : ||  |:|:  |: :|: | :|||:  :: ::  |     |      | ||
Db       3165 ---KTQAGFADGAPHYVAFYSNATGVWLYVDDQLQQMKPHRGPPPELQPQPEGPPRLLLG 3221

Qy        499 G-------GHFEGCISNVLVQRFSQSPEVLDL---------------------------- 523
               |         :| |||||| |||       | ||
Db       3222 GLPESGTIYNFSGCISNVFVQRLLGPQRVFDLQQNLGSVNVSTGCAPALQAQTPGLGPRQ 3281

Qy        524 ASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
               ||: ::: |    | |  || |   :   :|
Db       3282 ASRRSRQPARHPACML--PPHLRTTRDSYQF 3310


Search completed: February 22, 2005, 08:18:47
Job time : 107.16 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:19:00 ; Search time 75.7216 Seconds
(without alignments)
2441.722 Million cell updates/sec

Title: US-10-817-423-4
Perfect score: 2940
Sequence: 1 MRFNGKSGVEVRLPNDLEDL.....MLFKSPKRFNKGRIFNVNQL 565

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2940	100.0	1694	15	US-10-603-725-12	Sequence 12, Appl
2	2940	100.0	1725	15	US-10-603-725-10	Sequence 10, Appl
3	2439	83.0	1693	15	US-10-603-725-4	Sequence 4, Appli
4	2439	83.0	1693	15	US-10-603-725-8	Sequence 8, Appli
5	2439	83.0	1713	14	US-10-171-311-113	Sequence 113, App
6	2439	83.0	1713	15	US-10-372-683-10	Sequence 10, Appl
7	2439	83.0	1713	15	US-10-603-725-6	Sequence 6, Appli
8	2439	83.0	1724	15	US-10-603-725-2	Sequence 2, Appli
9	717.5	24.4	3597	15	US-10-037-417-6	Sequence 6, Appli
10	717.5	24.4	3600	15	US-10-037-417-2	Sequence 2, Appli
11	717	24.4	3690	15	US-10-112-944-347	Sequence 347, App
12	715	24.3	1634	15	US-10-037-417-49	Sequence 49, Appl
13	715	24.3	1677	15	US-10-112-944-801	Sequence 801, App
14	715	24.3	3695	15	US-10-312-352-22	Sequence 22, Appl
15	715	24.3	3696	15	US-10-312-088-31	Sequence 31, Appl
16	715	24.3	3705	15	US-10-312-088-30	Sequence 30, Appl
17	712	24.2	1640	15	US-10-037-417-8	Sequence 8, Appli
18	712	24.2	3695	14	US-10-037-182-2	Sequence 2, Appli
19	694	23.6	1816	15	US-10-372-683-4	Sequence 4, Appli
20	688	23.4	1823	15	US-10-363-616-457	Sequence 457, App
21	686	23.3	1581	16	US-10-408-765A-154	Sequence 154, App
22	685	23.3	953	9	US-09-845-583-4	Sequence 4, Appli
23	685	23.3	953	15	US-10-037-417-50	Sequence 50, Appl
24	683	23.2	1816	14	US-10-299-058-2	Sequence 2, Appli
25	681	23.2	1816	14	US-10-299-058-4	Sequence 4, Appli
26	681	23.2	3635	9	US-09-845-583-2	Sequence 2, Appli
27	681	23.2	3635	14	US-10-037-182-4	Sequence 4, Appli
28	681	23.2	3635	15	US-10-037-417-47	Sequence 47, Appl
29	680	23.1	469	14	US-10-106-698-5877	Sequence 5877, Ap
30	578	19.7	908	15	US-10-037-417-4	Sequence 4, Appli
31	395	13.4	3712	13	US-10-108-605-103	Sequence 103, App
32	395	13.4	3712	15	US-10-037-417-48	Sequence 48, Appl
33	395	13.4	3712	15	US-10-037-417-51	Sequence 51, Appl
34	322.5	11.0	296	14	US-10-299-058-5	Sequence 5, Appli
35	322.5	11.0	296	14	US-10-299-058-6	Sequence 6, Appli
36	321	10.9	289	14	US-10-299-058-13	Sequence 13, Appl
37	298.5	10.2	3672	15	US-10-369-493-6146	Sequence 6146, Ap
38	280	9.5	3084	9	US-09-938-275-4	Sequence 4, Appli
39	280	9.5	3084	14	US-10-262-670-2	Sequence 2, Appli
40	270	9.2	3075	9	US-09-938-275-5	Sequence 5, Appli
41	252	8.6	3070	10	US-09-961-403-7	Sequence 7, Appli
42	222.5	7.6	2823	15	US-10-369-493-5220	Sequence 5220, Ap
43	222.5	7.6	2823	15	US-10-369-493-5221	Sequence 5221, Ap
44	213.5	7.3	1399	15	US-10-187-975-26	Sequence 26, Appl
45	213.5	7.3	1438	15	US-10-187-975-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-10-603-725-12
; Sequence 12, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boutand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1694
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-603-725-12

Query Match 100.0%; Score 2940; DB 15; Length 1694;
Best Local Similarity 100.0%; Pred. No. 7.6e-240;
Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 810

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 870

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 930

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        931 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 990

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 1050

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 1110

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 1170

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 1230

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 1290

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              |||||||||||||||||||||||||
Db       1291 KPPFLMLFKSPKRFNKGRIFNVNQL 1315


RESULT 2
US-10-603-725-10
; Sequence 10, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
;  APPLICANT: Boutand, Ariel
;  TITLE OF INVENTION: Recombinant Laminin 5
;  FILE REFERENCE: 99-274-C
;  CURRENT APPLICATION NUMBER: US/10/603,725
;  CURRENT FILING DATE:  2003-06-25
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 1725
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-603-725-10

  Query Match            100.0%;  Score 2940;  DB 15;  Length 1725;
  Best Local Similarity  100.0%;  Pred. No. 7.8e-240;
  Matches  565;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 841

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 901

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRPPPYKGCIELDDLNEN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRPPPYKGCIELDDLNEN 961

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 1021

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 1081

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 1141

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 1201

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 1261

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 1321

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              |||||||||||||||||||||||||
Db       1322 KPPFLMLFKSPKRFNKGRIFNVNQL 1346


RESULT 3
US-10-603-725-4
; Sequence 4, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
;  APPLICANT: Boutand, Ariel
;  TITLE OF INVENTION: Recombinant Laminin 5
;  FILE REFERENCE: 99-274-C
;  CURRENT APPLICATION NUMBER: US/10/603,725
;  CURRENT FILING DATE:  2003-06-25
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1693
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-603-725-4

  Query Match            83.0%;  Score 2439;  DB 15;  Length 1693;
  Best Local Similarity  81.9%;  Pred. No. 2.6e-197;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        751 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 810

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        811 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 870

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: |||||||||:||||| ||||||||||||||||||
Db        871 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 930

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        931 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 990

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db        991 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1050

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::   |:||:||||||||||||||||||||||:|||||||||||||||||
Db       1051 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1110

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||:||||||||:|||:| :| ||   | ||||||||||| ||:||
Db       1111 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1170

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1171 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1230

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||||| :|||||||| ||| | ||||||| | | |:| ||||||||
```

```
Db       1231 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1290

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1291 KPPFLMLLKGSTRFNKTKTFRINQL 1315


RESULT 4
US-10-603-725-8
; Sequence 8, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
;  APPLICANT: Boutand, Ariel
;  TITLE OF INVENTION: Recombinant Laminin 5
;  FILE REFERENCE: 99-274-C
;  CURRENT APPLICATION NUMBER: US/10/603,725
;  CURRENT FILING DATE:  2003-06-25
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 1693
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-603-725-8

  Query Match           83.0%;  Score 2439;  DB 15;  Length 1693;
  Best Local Similarity   81.9%;  Pred. No. 2.6e-197;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        751 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 810

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        811 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 870

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :||||||||||: |||||||||||:||||| ||||||||||||||||
Db        871 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 930

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        931 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 990

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db        991 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1050

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||:|||||||||||||||||||
Db       1051 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1110

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:|||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1111 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1170

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1171 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1230

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||||| :|||||||| ||| | ||||||| | | |:| |||||||
Db       1231 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1290

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1291 KPPFLMLLKGSTRFNKTKTFRINQL 1315


RESULT 5
US-10-171-311-113
; Sequence 113, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
;  APPLICANT: Schlegel, Robert
;  APPLICANT:  Chen, Yan
;  APPLICANT:  Zhao, Xumei
;  APPLICANT:  Monahan, John
;  APPLICANT:  Kamatkar, Shubhangi
;  APPLICANT:  Glatt, Karen
;  APPLICANT:  Gannavarapu, Manjula
;  APPLICANT:  Hoersh, Sebastian
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
;  TITLE OF INVENTION:  OF CERVICAL CANCER
;  FILE REFERENCE: MRI-035
;  CURRENT APPLICATION NUMBER: US/10/171,311
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: US 60/298,159
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,155
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/335,936
;  PRIOR FILING DATE: 2001-11-14
;  NUMBER OF SEQ ID NOS: 238
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 113
;   LENGTH: 1713
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-171-311-113

  Query Match           83.0%;  Score 2439;  DB 14;  Length 1713;
  Best Local Similarity   81.9%;  Pred. No. 2.6e-197;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :||||||||||: |||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||:|||||||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:|||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||||| :|||||||| ||| | ||||||| | | |:| |||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQL 1335
```

```
RESULT 6
US-10-372-683-10
; Sequence 10, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
;  APPLICANT: GERRITSEN, MARY E.
;  APPLICANT:  PEALE JR., FRANKLIN V.
;  APPLICANT:  WU, THOMAS D.
;  TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
;  FILE REFERENCE: P1928R1P1
;  CURRENT APPLICATION NUMBER: US/10/372,683
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US 10/271,690
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/344,534
;  PRIOR FILING DATE: 2001-10-18
;  NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 10
;   LENGTH: 1713
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-372-683-10

  Query Match             83.0%;  Score 2439;  DB 15;  Length 1713;
  Best Local Similarity   81.9%;  Pred. No. 2.6e-197;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||: |||||||:||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::||||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| |||||||||||||||||||||||||||||:|||:|| | | ||||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||:|||||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::||||||| :||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 7
US-10-603-725-6
; Sequence 6, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
;  APPLICANT: Boutand, Ariel
;  TITLE OF INVENTION: Recombinant Laminin 5
;  FILE REFERENCE: 99-274-C
;  CURRENT APPLICATION NUMBER: US/10/603,725
;  CURRENT FILING DATE:  2003-06-25
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 1713
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-603-725-6

  Query Match             83.0%;  Score 2439;  DB 15;  Length 1713;
  Best Local Similarity   81.9%;  Pred. No. 2.6e-197;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||: |||||||:||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::||||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| |||||||||||||||||||||||||||||:|||:|| | | ||||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||:|||||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::||||||| :||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 8
US-10-603-725-2
; Sequence 2, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
;  APPLICANT: Boutand, Ariel
;  TITLE OF INVENTION: Recombinant Laminin 5
;  FILE REFERENCE: 99-274-C
;  CURRENT APPLICATION NUMBER: US/10/603,725
;  CURRENT FILING DATE:  2003-06-25
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
```

```
;   LENGTH: 1724
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-603-725-2

  Query Match             83.0%;  Score 2439;  DB 15;  Length 1724;
  Best Local Similarity   81.9%;  Pred. No. 2.6e-197;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||: |||||||:|||||||||||:|||| 
Db        782 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 841

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||: 
Db        842 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 901

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| |||||||||||||||| 
Db        902 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 961

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||:||||:|| | | ||||||| 
Db        962 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1021

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | ||||| 
Db       1022 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1081

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||:|||||||||||||||| 
Db       1082 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1141

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:|||||||:|||:| :| ||  | ||||||||| ||:|| 
Db       1142 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1201

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              || :| ||||||:||||| ||  |||||| ||||||||:|||||| |||||||||:|| 
Db       1202 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1261

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||||| :|||||||| ||| | ||||||| | | |:| |||||||| 
Db       1262 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1321

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1322 KPPFLMLLKGSTRFNKTKTFRINQL 1346


RESULT 9
US-10-037-417-6
; Sequence 6, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
;  APPLICANT: Kekuda, Ramesh
;  APPLICANT:  Alsobrook II, John P
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Lepley, Denise M
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Li, Li
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Edinger, Shlomit R
;  APPLICANT:  Sciore, Paul
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Rothenberg, Mark
;  APPLICANT:  Stone, David J
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Anderson, David W
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Miller, Charles E
;  APPLICANT:  Eisen, Andrew J
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-235
;  CURRENT APPLICATION NUMBER: US/10/037,417
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: 60/260,018
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: 60/260,360
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/272,411
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/272,817
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: 60/291,186
;  PRIOR FILING DATE: 2001-05-15
;  PRIOR APPLICATION NUMBER: 60/303,231
;  PRIOR FILING DATE: 2001-07-05
;  PRIOR APPLICATION NUMBER: 60/305,060
;  PRIOR FILING DATE: 2001-07-12
;  PRIOR APPLICATION NUMBER: 60/318,405
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: 60/318,700
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 3597
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-037-417-6

  Query Match             24.4%;  Score 717.5;  DB 15;  Length 3597;
  Best Local Similarity   31.7%;  Pred. No. 1.1e-50;
  Matches  200;  Conservative  100;  Mismatches  222;  Indels  109;  Gaps   22;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |:|||:|||::| | || ||  ||:|  :|| |:      |||| ||||:|:: |: ||:| 
Db       2712 MKFNGRSGVQLRTPRDLADLAAYTALKFYLQGPEPEPGQGTEDRFVMYMGSRQATGDYMG 2771

Qy         61 MAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE--- 116
              ::: | ::  || ||:   | : ||: : |          |   |  ||  :: | | 
Db       2772 VSLRDKKVHWVYQLGEAGPAVLSIDEDIGEQ------FAAVSLDRTLQFGHMSVTVERQM 2825

Qy        117 --ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIEL 174
                |      ||      ||      |||| |:| |||||||  |  |  |||| |:||||: 
Db       2826 IQETKGDTVAPGA---EG-----LLNLRPDDFVFYVGGYPSTFTPPPLLRFPGYRGCIEM 2877

Qy        175 DDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPN-AP 228
              | ||| |:|||||: || |:|    || | |        :| :| :|||:|||      : 
Db       2878 DTLNEEVVSLYNFERTFQLDTAVDRPCARSKSTGDPWLTDGSYLDGTGFARISFDSQIST 2937

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPP----- 275
              | | ::      |:||| : |  |: | :::|:|:: |   :         :||
Db       2938 TKRFEQELRLVSYSGVLFFLKQQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPPLTS 2997

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNER---SVRIEGEIFDFSTYYLGGIP-- 330
              | |:           : :|  :||: : |       ||  : ::     |||||:|
Db       2998 ASKAIQ-----------VFLLGGSRKRVLVRVERATVYSVEQDNDLELADAYYLGGVPPD 3046

Qy        331 -IAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGG 386
              :    |   :  : :||:| :|    |   : ||| | ||:  |: |  :  :  :|   | 
Db       3047 QLPSLRRLFPTGGSVRGCVKGIKALGKYVDLKRLN-TTGVSAGCTADLLVGRAMTFHGHG 3105

Qy        387 --QMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNI 444
                ::: :|:  | |      ||| : | |  |   :          |:|: | |:  | : 
Db       3106 FLRLALSNV-APLTGNVYSGFGFHSAQDSALLYYRASPVRPHQVSLQQGRVSLQLLRTEV 3164
```

```
Qy        445 PIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQV--LRRNQRLPSFSNAQQS----LRLG 498
              |:   : ||  |:|:  |: :|: | :|||:  :: ::  |      |       | ||
Db       3165 ---KTQAGFADGAPHYVAFYSNATGVWLYVDDQLQQMKPHRGPPPELQPQPEGPPRLLLG 3221

Qy        499 G-------GHFEGCISNVLVQRFSQSPEVLDL---------------------------- 523
              |       :| |||||| |||      | ||
Db       3222 GLPESGTIYNFSGCISNVFVQRLLGPQRVFDLQQNLGSVNVSTGCAPALQAQTPGLGPRQ 3281

Qy        524 ASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
              ||: ::: |    | |  || |   :   :|
Db       3282 ASRRSRQPARHPACML--PPHLRTTRDSYQF 3310
```

RESULT 10
US-10-037-417-2
; Sequence 2, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3600
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-037-417-2

Query Match 24.4%; Score 717.5; DB 15; Length 3600;
Best Local Similarity 31.7%; Pred. No. 1.1e-50;
Matches 200; Conservative 100; Mismatches 222; Indels 109; Gaps 22;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |:|||:|||::| | || ||  ||:|  :|| |:     |||| ||||:|:: |: ||:|
Db       2715 MKFNGRSGVQLRTPRDLADLAAYTALKFYLQGPEPEPGQGTEDRFVMYMGSRQATGDYMG 2774

Qy         61 MAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE--- 116
              ::: | ::  || ||:   | : ||: : |          |   |  ||  :: | |
Db       2775 VSLRDKKVHWVYQLGEAGPAVLSIDEDIGEQ------FAAVSLDRTLQFGHMSVTVERQM 2828

Qy        117 --ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIEL 174
                |     ||     ||      |||| |:| |||||||  |  |  |||| |:||||:
Db       2829 IQETKGDTVAPGA---EG-----LLNLRPDDFVFYVGGYPSTFTPPPLLRFPGYRGCIEM 2880

Qy        175 DDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPN-AP 228
              | ||| |:|||||: || |:|    || | |       :| :| :|||:|||      :
Db       2881 DTLNEEVVSLYNFERTFQLDTAVDRPCARSKSTGDPWLTDGSYLDGTGFARISFDSQIST 2940

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPP----- 275
              | | ::     |:||| : |  |: | :::|:|:: |   :         :||
Db       2941 TKRFEQELRLVSYSGVLFFLKQQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPPLTS 3000

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNER---SVRIEGEIFDFSTYYLGGIP-- 330
              | |:          :  :|  :||: : |       ||  : ::     |||||:|
Db       3001 ASKAIQ-----------VFLLGGSRKRVLVRVERATVYSVEQDNDLELADAYYLGGVPPD 3049

Qy        331 -IAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGG 386
              :   |   :  : :||:| :|    |   : ||| | ||:  |: |  : |  :|    |
Db       3050 QLPSLRRLFPTGGSVRGCVKGIKALGKYVDLKRLN-TTGVSAGCTADLLVGRAMTFHGHG 3108

Qy        387 --QMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNI 444
                ::: :|:  | |       ||| : | |  |     :       |:|: | : |     : :
Db       3109 FLRLALSNV-APLTGNVYSGFGFHSAQDSALLYYRASPVRPHQVSLQQGRVSLQLLRTEV 3167

Qy        445 PIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQV--LRRNQRLPSFSNAQQS----LRLG 498
              |:   : ||  |:|:  |: :|: | :|||:  :: ::  |      |       | ||
Db       3168 ---KTQAGFADGAPHYVAFYSNATGVWLYVDDQLQQMKPHRGPPPELQPQPEGPPRLLLG 3224

Qy        499 G-------GHFEGCISNVLVQRFSQSPEVLDL---------------------------- 523
              |       :| |||||| |||      | ||
Db       3225 GLPESGTIYNFSGCISNVFVQRLLGPQRVFDLQQNLGSVNVSTGCAPALQAQTPGLGPRQ 3284

Qy        524 ASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
              ||: ::: |    | |  || |   :   :|
Db       3285 ASRRSRQPARHPACML--PPHLRTTRDSYQF 3313
```

RESULT 11
US-10-112-944-347
; Sequence 347, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28

```
;  PRIOR APPLICATION NUMBER: US 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: US 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: US 09/515,126
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: US 09/519,705
;  PRIOR FILING DATE: 2000-03-07
;  PRIOR APPLICATION NUMBER: US 09/540,217
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: US 09/552,929
;  PRIOR FILING DATE: 2000-04-18
;  PRIOR APPLICATION NUMBER: US 09/577,408
;  PRIOR FILING DATE: 2000-05-18
;  NUMBER OF SEQ ID NOS: 924
;  SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 347
;   LENGTH: 3690
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-112-944-347

  Query Match           24.4%;  Score 717;  DB 15;  Length 3690;
  Best Local Similarity   31.7%;  Pred. No. 1.3e-50;
  Matches  201;  Conservative  101;  Mismatches  219;  Indels  114;  Gaps   23;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |:|||:|||::| | || ||  ||:|  :|| |:     |||| ||||:|:: |: ||:|
Db       2737 MKFNGRSGVQLRTPRDLADLAAYTALKFYLQGPEPEPGQGTEDRFVMYMGSRQATGDYMG 2796

Qy         61 MAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE--- 116
              ::: | ::  || ||:   | : ||: : |          |   |  ||  :: | |
Db       2797 VSLRDKKVHWVYQLGEAGPAVLSIDEDIGEQ------FAAVSLDRTLQFGHMSVTVERQM 2850

Qy        117 --ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIEL 174
                |      ||      ||     |||| |:| ||||||||  |   |  |||| |:||||:
Db       2851 IQETKGDTVAPGA---EG-----LLNLRPDDFVFYVGGYPSTFTPPPLLRFPGYRGCIEM 2902

Qy        175 DDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPN-AP 228
              | ||| |:|||||: || |:|    || | |       :| :| :|||:|||      :
Db       2903 DTLNEEVVSLYNFERTFQLDTAVDRPCARSKSTGDPWLTDGSYLDGTGFARISFDSQIST 2962

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPP----- 275
              | | ::      |:||| : |  |: | :::|:|:: |   :         :||
Db       2963 TKRFEQELRLVSYSGVLFFLKQQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPPLTS 3022

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNER---SVRIEGEIFDFSTYYLGGI--- 329
              | |:           :  :|  :||: : |      ||  : ::      |||||:
Db       3023 ASKAIQ----------VFLLGGSRKRVLVRVERATVYSVEQDNDLELADAYYLGGVPPD 3071

Qy        330 --PIAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSR 384
                | ::|  |  :  : :||:| :|    |   : ||| | ||:  |: |  : |  :|
Db       3072 QLPPSLRRLFP-TGGSVRGCVKGIKALGKYVDLKRLN-TTGVSAGCTADLLVGRAMTFHG 3129

Qy        385 GG--QMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDS 442
              |  ::: :|:  | |      ||| : | | |    :      |:|: | : |    :
Db       3130 HGFLRLALSNV-APLTGNVYSGFGFHSAQDSALLYYRASPDGLCQVSLQQGRVSLQLLRT 3188

Qy        443 NIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQV--LRRNQRLPSFSNAQQS----LR 496
              :   |:   : ||  |:|:  |: :|: | :|||:  :: ::  |     |       |
Db       3189 EV---KTQAGFADGAPHYVAFYSNATGVWLYVDDQLQQMKPHRGPPPELQPQPEGPPRLL 3245

Qy        497 LGG-------GHFEGCISNVLVQRFSQSPEVLDL------------------------- 523
              |||         :| |||||| |||      | ||
Db       3246 LGGLPESGTIYNFSGCISNVFVQRLLGPQRVFDLQQNLGSVNVSTGCAPALQAQTPGLGP 3305

Qy        524 ----ASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
                  ||: ::: |    | |  || |   :  :|
Db       3306 RGLQASRRSRQPARHPACML--PPHLRTTRDSYQF 3338
```

```
RESULT 12
US-10-037-417-49
; Sequence 49, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
;  APPLICANT: Kekuda, Ramesh
;  APPLICANT:  Alsobrook II, John P
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Lepley, Denise M
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Li, Li
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Edinger, Shlomit R
;  APPLICANT:  Sciore, Paul
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Rothenberg, Mark
;  APPLICANT:  Stone, David J
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Anderson, David W
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Miller, Charles E
;  APPLICANT:  Eisen, Andrew J
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-235
;  CURRENT APPLICATION NUMBER: US/10/037,417
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: 60/260,018
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: 60/260,360
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/272,411
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/272,817
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: 60/291,186
;  PRIOR FILING DATE: 2001-05-15
;  PRIOR APPLICATION NUMBER: 60/303,231
;  PRIOR FILING DATE: 2001-07-05
;  PRIOR APPLICATION NUMBER: 60/305,060
;  PRIOR FILING DATE: 2001-07-12
;  PRIOR APPLICATION NUMBER: 60/318,405
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: 60/318,700
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
;   LENGTH: 1634
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-037-417-49

  Query Match           24.3%;  Score 715;  DB 15;  Length 1634;
  Best Local Similarity   33.1%;  Pred. No. 5.5e-51;
  Matches  194;  Conservative   96;  Mismatches  214;  Indels   82;  Gaps   21;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |:|||:|||::| | || ||  ||:|  :|| |:     |||| ||||:|:: |: ||:|
Db        676 MKFNGRSGVQLRTPRDLADLAAYTALKFYLQGPEPEPGQGTEDRFVMYMGSRQATGDYMG 735

Qy         61 MAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE--- 116
              ::: | ::  || ||:   | : ||: : |          |   |  ||  :: | |
Db        736 VSLRDKKVHWVYQLGEAGPAVLSIDEDIGEQ------FAAVSLDRTLQFGHMSVTVERQM 789
```

```
Qy        117 --ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIEL 174
                  |    ||     ||     |||| |:| ||||||||  |  |  |||| |:||||:
Db        790 IQETKGDTVAPGA---EG-----LLNLRPDDFVFYVGGYPSTFTPPPLLRFPGYRGCIEM 841

Qy        175 DDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPN-AP 228
              | ||| |:|||||: || |:|    || | |       :| :| :|||:|||      :
Db        842 DTLNEEVVSLYNFERTFQLDTAVDRPCARSKSTGDPWLTDGSYLDGTGFARISFDSQIST 901

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPP----- 275
                | | ::     |:||| : |  |: | :::|:|:: |   :        :||
Db        902 TKRFEQELRLVSYSGVLFFLKQQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPPLTS 961

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNER---SVRIEGEIFDFSTYYLGGI--- 329
              | |:          :  :|  :||: : |      ||  : ::     |||||:
Db        962 ASKAIQ----------VFLLGGSRKRVLVRVERATVYSVEQDNDLELADAYYLGGVPPD 1010

Qy        330 --PIAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSR 384
                | ::|  |  :  : :||:| :|   |   : ||| | ||:  |: |  : |  :|
Db       1011 QLPPSLRRLFP-TGGSVRGCVKGIKALGKYVDLKRLN-TTGVSAGCTADLLVGRAMTFHG 1068

Qy        385 GG--QMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDS 442
              |  ::: :|:  | |      ||| : | |  |     :      |:|: | : |   :
Db       1069 HGFLRLALSNV-APLTGNVYSGFGFHSAQDSALLYYRASPDGLCQVSLQQGRVSLQLLRT 1127

Qy        443 NIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQV--LRRNQRLPSFSNAQQS----LR 496
              :   |:   : ||  |:|:  |: :|: | :|||:  :: ::  |      |      |
Db       1128 EV---KTQAGFADGAPHYVAFYSNATGVWLYVDDQLQQMKPHRGPPPELQPQPEGPPRLL 1184

Qy        497 LGG-------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLG 535
              |||        :| |||||| |||      | ||       : | |
Db       1185 LGGLPESGTIYNFSGCISNVFVQRLLGPQRVFDLQQNLGSVNVSTG 1230


RESULT 13
US-10-112-944-801
; Sequence 801, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Yang, Yonghong
;  APPLICANT:  Weng, Gezhi
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Ghosh, Malabika
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Zhiwei
;  TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
;  TITLE OF INVENTION:  Secreted Polypeptides
;  FILE REFERENCE: 805A
;  CURRENT APPLICATION NUMBER: US/10/112,944
;  CURRENT FILING DATE:  2002-03-28
;  PRIOR APPLICATION NUMBER: US 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: US 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: US 09/515,126
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: US 09/519,705
;  PRIOR FILING DATE: 2000-03-07
;  PRIOR APPLICATION NUMBER: US 09/540,217
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: US 09/552,929
;  PRIOR FILING DATE: 2000-04-18
;  PRIOR APPLICATION NUMBER: US 09/577,408
;  PRIOR FILING DATE: 2000-05-18
;  NUMBER OF SEQ ID NOS: 924
;  SOFTWARE: pt_FL_genes Version 5.0

; SEQ ID NO 801
;   LENGTH: 1677
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-112-944-801

  Query Match             24.3%;  Score 715;  DB 15;  Length 1677;
  Best Local Similarity   33.1%;  Pred. No. 5.7e-51;
  Matches  194;  Conservative   96;  Mismatches  214;  Indels   82;  Gaps   21;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |:|||:|||::| | || ||  ||:|  :|| |:      |||| ||||:|:: |: ||:|
Db        687 MKFNGRSGVQLRTPRDLADLAAYTALKFYLQGPEPEPGQGTEDRFVMYMGSRQATGDYMG 746

Qy         61 MAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE--- 116
              ::: | ::  || ||:   | : ||: : |          |   |  ||  :: | |
Db        747 VSLRDKKVHWVYQLGEAGPAVLSIDEDIGEQ------FAAVSLDRTLQFGHMSVTVERQM 800

Qy        117 --ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIEL 174
                  |    ||     ||     |||| |:| |||||||||  |  |  |||| |:||||:
Db        801 IQETKGDTVAPGA---EG-----LLNLRPDDFVFYVGGYPSTFTPPPLLRFPGYRGCIEM 852

Qy        175 DDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPN-AP 228
              | ||| |:|||||: || |:|    || | |       :| :| :|||:|||      :
Db        853 DTLNEEVVSLYNFERTFQLDTAVDRPCARSKSTGDPWLTDGSYLDGTGFARISFDSQIST 912

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPP----- 275
                | | ::     |:||| : |  |: | :::|:|:: |   :        :||
Db        913 TKRFEQELRLVSYSGVLFFLKQQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPPLTS 972

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNER---SVRIEGEIFDFSTYYLGGI--- 329
              | |:          :  :|  :||: : |      ||  : ::     |||||:
Db        973 ASKAIQ----------VFLLGGSRKRVLVRVERATVYSVEQDNDLELADAYYLGGVPPD 1021

Qy        330 --PIAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSR 384
                | ::|  |  :  : :||:| :|   |   : ||| | ||:  |: |  : |  :|
Db       1022 QLPPSLRRLFP-TGGSVRGCVKGIKALGKYVDLKRLN-TTGVSAGCTADLLVGRAMTFHG 1079

Qy        385 GG--QMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDS 442
              |  ::: :|:  | |      ||| : | |  |     :      |:|: | : |   :
Db       1080 HGFLRLALSNV-APLTGNVYSGFGFHSAQDSALLYYRASPDGLCQVSLQQGRVSLQLLRT 1138

Qy        443 NIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQV--LRRNQRLPSFSNAQQS----LR 496
              :   |:   : ||  |:|:  |: :|: | :|||:  :: ::  |      |      |
Db       1139 EV---KTQAGFADGAPHYVAFYSNATGVWLYVDDQLQQMKPHRGPPPELQPQPEGPPRLL 1195

Qy        497 LGG-------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLG 535
              |||        :| |||||| |||      | ||       : | |
Db       1196 LGGLPESGTIYNFSGCISNVFVQRLLGPQRVFDLQQNLGSVNVSTG 1241


RESULT 14
US-10-312-352-22
; Sequence 22, Application US/10312352
; Publication No. US20040053824A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom
;  APPLICANT:  YUE, Henry; AZIMZAI, Yalda
;  APPLICANT:  HE, Ann; BATRA, Sajeev
;  APPLICANT:  LO, Terence P.; NGUYEN, Danniel B.
;  APPLICANT:  BURRILL, John D.; MARCUS, Gregory A.
;  APPLICANT:  ZINGLER, Kurt A.; GANDHI, Ameena R.
;  APPLICANT:  LAL, Preeti G.; KEARNEY, Liam
;  APPLICANT:  BURFORD, Neil; YAO, Monique G.
;  APPLICANT:  CHAWLA, Narinder K.; ELLIOT, Vicki S.
;  APPLICANT:  ARVIZU, Chandra S.; KHAN, Farrah A.
;  APPLICANT:  BAUGHN, Mariah R.; HAFALIA, April, J.A.
;  APPLICANT:  POLICKY, Jennifer L.; AU-YOUNG, Janice K.
;  APPLICANT:  LU, Yan; BOROWSKY, Mark L.
;  APPLICANT:  LU, Dyung Aina M.; RAMKUMAR, Jayalaxmi
;  APPLICANT:  YANG, Junming; GURURAJAN, Rajagopal
;  APPLICANT:  WARREN, Bridget A.; GIETZEN, Kimberly J.
;  APPLICANT:  XU, Yuming; KALLICK, Deborah A.
```

```
;  APPLICANT:  LEE, Ernestine A.; THANGAVELU, Kavitha
;  APPLICANT:  DELEGEANE, Angelo M.; LEE, Sally
;  TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
;  FILE REFERENCE: PF-0794 USN
;  CURRENT APPLICATION NUMBER: US/10/312,352
;  CURRENT FILING DATE:  2002-12-18
;  PRIOR APPLICATION NUMBER: PCT/US01/21067
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/215,454
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 60/219,462
;  PRIOR FILING DATE: 2000-07-18
;  PRIOR APPLICATION NUMBER: US 60/240,111
;  PRIOR FILING DATE: 2000-10-12
;  PRIOR APPLICATION NUMBER: US 60/240,106
;  PRIOR FILING DATE: 2000-10-12
;  PRIOR APPLICATION NUMBER: US 60/244,021
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: US 60/248,887
;  PRIOR FILING DATE: 2000-11-14
;  PRIOR APPLICATION NUMBER: US 60/249,570
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: PERL Program
; SEQ ID NO 22
;   LENGTH: 3695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040053824A1 6382722CD1
US-10-312-352-22

  Query Match            24.3%;  Score 715;  DB 15;  Length 3695;
  Best Local Similarity  33.1%;  Pred. No. 1.9e-50;
  Matches  194;  Conservative   96;  Mismatches  214;  Indels   82;  Gaps   21;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |:|||:|||::| | || ||  ||:|  :|| |:     |||| ||||:|:: |:.||:|
Db       2737 MKFNGRSGVQLRTPRDLADLAAYTALKFYLQGPEPEPGQGTEDRFVMYMGSRQATGDYMG 2796

Qy         61 MAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE--- 116
              ::: | ::  || ||:   | : ||: : |          |   |  ||  :: | |
Db       2797 VSLRDKKVHWVYQLGEAGPAVLSIDEDIGEQ------FAAVSLDRTLQFGHMSVTVERQM 2850

Qy        117 --ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIEL 174
                |      ||      ||      |||| |:| |||||||  |  |  |||| |:||||:
Db       2851 IQETKGDTVAPGA---EG-----LLNLRPDDFVFYVGGYPSTFTPPPLLRFPGYRGCIEM 2902

Qy        175 DDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPN-AP 228
              | ||| |:|||||: || |:|    || | |       :| :| :|||:|||      :
Db       2903 DTLNEEVVSLYNFERTFQLDTAVDRPCARSKSTGDPWLTDGSYLDGTGFARISFDSQIST 2962

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPP----- 275
                | | ::      |:||| : |  |: | :::|:|:: |   :         :||
Db       2963 TKRFEQELRLVSYSGVLFFLKQQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPPLTS 3022

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNER---SVRIEGEIFDFSTYYLGGI--- 329
                | |:          :  :|  :||: : |      ||  : ::     |||||:
Db       3023 ASKAIQ-----------VFLLGGSRKRVLVRVERATVYSVEQDNDLELADAYYLGGVPPD 3071

Qy        330 --PIAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSR 384
                | ::|  |  :  : :||:| :|   |   : ||| | ||:  |: |  : |   :|
Db       3072 QLPPSLRRLFP-TGGSVRGCVKGIKALGKYVDLKRLN-TTGVSAGCTADLLVGRAMTFHG 3129

Qy        385 GG--QMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDS 442
               |  ::: :|:  | |       ||| : | |  |    :      |:|: | : |    :
Db       3130 HGFLRLALSNV-APLTGNVYSGFGFHSAQDSALLYYRASPDGLCQVSLQQGRVSLQLLRT 3188

Qy        443 NIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQV--LRRNQRLPSFSNAQQS----LR 496
               :   |:   : ||  |:|:  |: :|: | :|||:  :: ::  |      |      |
Db       3189 EV---KTQAGFADGAPHYVAFYSNATGVWLYVDDQLQQMKPHRGPPPELQPQPEGPPRLL 3245
```

```
Qy         497 LGG-------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLG 535
               |||        :| |||||| |||       | ||       : | |
Db        3246 LGGLPESGTIYNFSGCISNVFVQRLLGPQRVFDLQQNLGSVNVSTG 3291


RESULT 15
US-10-312-088-31
; Sequence 31, Application US/10312088
; Publication No. US20030219862A1
; GENERAL INFORMATION:
;  APPLICANT: Agarwal, Pankaj
;  APPLICANT:  Cogswell, John P.
;  APPLICANT:  Kabnic, Karen S.
;  APPLICANT:  Lai, Ying-Ta
;  APPLICANT:  Martensen, Shelby A.
;  APPLICANT:  Murdock, Paul R.
;  APPLICANT:  Smith, Randall P.
;  APPLICANT:  Strum, Jay C.
;  APPLICANT:  Xiang, Zhaoying
;  APPLICANT:  Xie, Qing
;  APPLICANT:  Rizni, Safia K.
;  TITLE OF INVENTION: NOVEL COMPOUNDS
;  FILE REFERENCE: GP50029
;  CURRENT APPLICATION NUMBER: US/10/312,088
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: PCT/US01/19929
;  PRIOR FILING DATE: 2001-06-22
;  PRIOR APPLICATION NUMBER: 60/213,161
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/213,156
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
;   LENGTH: 3696
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-312-088-31

  Query Match            24.3%;  Score 715;  DB 15;  Length 3696;
  Best Local Similarity  33.1%;  Pred. No. 1.9e-50;
  Matches  194;  Conservative   96;  Mismatches  214;  Indels   82;  Gaps   21;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |:|||:|||::| | || ||  ||:|  :|| |:     |||| ||||:|:: |:.||:|
Db       2738 MKFNGRSGVQLRTPRDLADLAAYTALKFYLQGPEPEPGQGTEDRFVMYMGSRQATGDYMG 2797

Qy         61 MAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE--- 116
              ::: | ::  || ||:   | : ||: : |          |   |  ||  :: | |
Db       2798 VSLRDKKVHWVYQLGEAGPAVLSIDEDIGEQ------FAAVSLDRTLQFGHMSVTVERQM 2851

Qy        117 --ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIEL 174
                |      ||      ||      |||| |:| |||||||  |  |  |||| |:||||:
Db       2852 IQETKGDTVAPGA---EG-----LLNLRPDDFVFYVGGYPSTFTPPPLLRFPGYRGCIEM 2903

Qy        175 DDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPN-AP 228
              | ||| |:|||||: || |:|    || | |       :| :| :|||:|||      :
Db       2904 DTLNEEVVSLYNFERTFQLDTAVDRPCARSKSTGDPWLTDGSYLDGTGFARISFDSQIST 2963

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPP----- 275
                | | ::      |:||| : |  |: | :::|:|:: |   :         :||
Db       2964 TKRFEQELRLVSYSGVLFFLKQQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPPLTS 3023

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNER---SVRIEGEIFDFSTYYLGGI--- 329
                | |:          :  :|  :||: : |      ||  : ::     |||||:
Db       3024 ASKAIQ-----------VFLLGGSRKRVLVRVERATVYSVEQDNDLELADAYYLGGVPPD 3072

Qy        330 --PIAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSR 384
                | ::|  |  :  : :||:| :|   |   : ||| | ||:  |: |  : |   :|
Db       3073 QLPPSLRRLFP-TGGSVRGCVKGIKALGKYVDLKRLN-TTGVSAGCTADLLVGRAMTFHG 3130

Qy        385 GG--QMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDS 442
               |  ::: :|:  | |       ||| : | |  |    :      |:|: | : |    :
```

```
Db       3131 HGFLRLALSNV-APLTGNVYSGFGFHSAQDSALLYYRASPDGLCQVSLQQGRVSLQLLRT 3189

Qy        443 NIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQV--LRRNQRLPSFSNAQQS----LR 496
              :   |:   : ||  |:|:  |: :|: | :|||:  :: ::  |     |      |
Db       3190 EV---KTQAGFADGAPHYVAFYSNATGVWLYVDDQLQQMKPHRGPPPELQPQPEGPPRLL 3246

Qy        497 LGG-------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLG 535
              |||        :| |||||| |||      | ||       : | |
Db       3247 LGGLPESGTIYNFSGCISNVFVQRLLGPQRVFDLQQNLGSVNVSTG 3292
```

Search completed: February 22, 2005, 08:44:42
Job time : 78.7216 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:13:40 ; Search time 26.3827 Seconds
(without alignments)
1598.653 Million cell updates/sec

Title: US-10-817-423-4
Perfect score: 2940
Sequence: 1 MRFNGKSGVEVRLPNDLEDL.....MLFKSPKRFNKGRIFNVNQL 565

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2940	100.0	1694	4	US-09-560-385A-12	Sequence 12, Appl
2	2940	100.0	1725	4	US-09-560-385A-10	Sequence 10, Appl
3	2439	83.0	1693	4	US-09-560-385A-4	Sequence 4, Appli
4	2439	83.0	1693	4	US-09-560-385A-8	Sequence 8, Appli
5	2439	83.0	1713	3	US-08-600-982-24	Sequence 24, Appl
6	2439	83.0	1713	4	US-09-560-385A-6	Sequence 6, Appli
7	2439	83.0	1713	4	US-09-538-092-1359	Sequence 1359, Ap
8	2439	83.0	1713	5	PCT-US94-10261A-24	Sequence 24, Appl
9	2439	83.0	1724	4	US-09-560-385A-2	Sequence 2, Appli
10	1310	44.6	770	1	US-08-445-135-2	Sequence 2, Appli
11	715	24.3	3647	4	US-09-949-016-10932	Sequence 10932, A
12	694	23.6	1792	4	US-09-561-818A-4	Sequence 4, Appli
13	694	23.6	1800	4	US-09-561-818A-8	Sequence 8, Appli
14	694	23.6	1816	4	US-09-561-818A-2	Sequence 2, Appli
15	694	23.6	1824	4	US-09-561-818A-6	Sequence 6, Appli
16	685	23.3	953	4	US-09-845-583A-4	Sequence 4, Appli
17	683	23.2	1792	4	US-09-561-818A-12	Sequence 12, Appl
18	683	23.2	1816	4	US-09-561-818A-10	Sequence 10, Appl
19	681	23.2	3635	4	US-09-845-583A-2	Sequence 2, Appli
20	302	10.3	3084	4	US-09-562-702A-12	Sequence 12, Appl
21	302	10.3	3106	4	US-09-562-702A-10	Sequence 10, Appl
22	297	10.1	1130	6	5444158-2	Patent No. 5444158
23	297	10.1	1130	6	5444158-2	Patent No. 5444158
24	294	10.0	1130	2	US-08-460-309-2	Sequence 2, Appli
25	294	10.0	1130	2	US-08-125-077-2	Sequence 2, Appli
26	294	10.0	3088	4	US-09-562-702A-8	Sequence 8, Appli
27	294	10.0	3089	4	US-09-562-702A-4	Sequence 4, Appli
28	294	10.0	3110	4	US-09-562-702A-2	Sequence 2, Appli
29	294	10.0	3110	4	US-09-562-702A-6	Sequence 6, Appli
30	294	10.0	3110	4	US-09-561-709B-7	Sequence 7, Appli
31	294	10.0	3110	4	US-09-917-254-86	Sequence 86, Appl
32	294	10.0	3110	4	US-09-949-016-5937	Sequence 5937, Ap
33	294	10.0	3111	2	US-08-460-309-4	Sequence 4, Appli
34	294	10.0	3111	2	US-08-125-077-4	Sequence 4, Appli
35	270	9.2	3075	2	US-08-460-309-5	Sequence 5, Appli
36	270	9.2	3075	2	US-08-125-077-5	Sequence 5, Appli
37	252	8.6	3070	4	US-09-961-403-7	Sequence 7, Appli
38	182	6.2	1384	4	US-09-949-016-7814	Sequence 7814, Ap
39	153	5.2	705	4	US-10-006-011A-3	Sequence 3, Appli
40	153	5.2	4391	4	US-10-006-011A-2	Sequence 2, Appli
41	144	4.9	1331	4	US-09-949-016-6861	Sequence 6861, Ap
42	144	4.9	1523	3	US-09-182-024A-2	Sequence 2, Appli
43	139	4.7	1384	4	US-08-826-134-2	Sequence 2, Appli
44	139	4.7	1384	4	US-09-949-016-6395	Sequence 6395, Ap
45	139	4.7	1525	3	US-09-191-647-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-560-385A-12
; Sequence 12, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Boutand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1694
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-560-385A-12

Query Match 100.0%; Score 2940; DB 4; Length 1694;
Best Local Similarity 100.0%; Pred. No. 8.1e-285;
Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 810

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 870

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 930

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 990

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 1050

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 1110

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 1170
```

```
Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 1230

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 1290

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              |||||||||||||||||||||||||
Db       1291 KPPFLMLFKSPKRFNKGRIFNVNQL 1315


RESULT 2
US-09-560-385A-10
; Sequence 10, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
;  APPLICANT:  Boutand, Ariel
;  TITLE OF INVENTION:  Recombinant Laminin 5
;  FILE REFERENCE:  99-274-C
;  CURRENT APPLICATION NUMBER: US/09/560,385A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 1725
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-560-385A-10

  Query Match            100.0%;  Score 2940;  DB 4;  Length 1725;
  Best Local Similarity  100.0%;  Pred. No. 8.3e-285;
  Matches  565;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 841

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 901

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 961

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 1021

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 1081

Qy        301 KRMWINVNERSVRIEGEIFDPSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 KRMWINVNERSVRIEGEIFDPSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 1141

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 1201

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 1261

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 1321

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              |||||||||||||||||||||||||
Db       1322 KPPFLMLFKSPKRFNKGRIFNVNQL 1346


RESULT 3
US-09-560-385A-4
; Sequence 4, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
;  APPLICANT:  Boutand, Ariel
;  TITLE OF INVENTION:  Recombinant Laminin 5
;  FILE REFERENCE:  99-274-C
;  CURRENT APPLICATION NUMBER: US/09/560,385A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1693
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-560-385A-4

  Query Match            83.0%;  Score 2439;  DB 4;  Length 1693;
  Best Local Similarity  81.9%;  Pred. No. 1.4e-234;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||: |||||||:|||||||||||||:||||
Db        751 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 810

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::||||||||||||||:||||| |||:
Db        811 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 870

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db        871 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 930

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        931 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 990

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db        991 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1050

Qy        301 KRMWINVNERSVRIEGEIFDPSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||:|||||||||||||||||
Db       1051 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1110

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              ||||||||||||||||||:|||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1111 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1170

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| |||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1171 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1230

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||||| :|||||||| ||| | |||||||  | | |:| ||||||||
Db       1231 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1290

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1291 KPPFLMLLKGSTRFNKTKTFRINQL 1315


RESULT 4
US-09-560-385A-8
; Sequence 8, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
;  APPLICANT:  Boutand, Ariel
;  TITLE OF INVENTION:  Recombinant Laminin 5
```

```
;  FILE REFERENCE:  99-274-C
;  CURRENT APPLICATION NUMBER: US/09/560,385A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 1693
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-560-385A-8

  Query Match             83.0%;  Score 2439;  DB 4;  Length 1693;
  Best Local Similarity   81.9%;  Pred. No. 1.4e-234;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||: |||||||:|||||||||||||:||||
Db        751 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 810

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        811 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 870

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db        871 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 930

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||:||||:|| | | |||||||
Db        931 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 990

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db        991 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1050

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||:|||||||||||||||||
Db       1051 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1110

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1111 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1170

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1171 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1230

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1231 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1290

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1291 KPPFLMLLKGSTRFNKTKTFRINQL 1315


RESULT 5
US-08-600-982-24
; Sequence 24, Application US/08600982
; Patent No. 6120991
;  GENERAL INFORMATION:
;    APPLICANT:  Carter, William G.
;    APPLICANT:  Gil, Susanna A.
;    APPLICANT:  Ryan, Maureen C.
;    TITLE OF INVENTION:  Epiligrin, an Epithelial Ligand for
;    TITLE OF INVENTION:  Integrins
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen, O'Connor, Johnson, and Kindness
;      STREET:  1420 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101-8100
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/600,982
;      FILING DATE:  02-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Shelton, Dennis K.
;      REGISTRATION NUMBER:  26,997
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 682-8100
;      TELEFAX:  (206) 224-0779
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1713 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;      DESCRIPTION:  E170 protein as translated from sequence
;      DESCRIPTION:  of FIGURES 15A-15F, and as shown also in FIGURES
;      DESCRIPTION:  19A-19R
US-08-600-982-24

  Query Match             83.0%;  Score 2439;  DB 3;  Length 1713;
  Best Local Similarity   81.9%;  Pred. No. 1.4e-234;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||: |||||||:|||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::|||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: ||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||||:|||||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:||||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 6
```

```
US-09-560-385A-6
; Sequence 6, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
;  APPLICANT:  Boutand, Ariel
;  TITLE OF INVENTION:  Recombinant Laminin 5
;  FILE REFERENCE:  99-274-C
;  CURRENT APPLICATION NUMBER: US/09/560,385A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 1713
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-560-385A-6

  Query Match             83.0%;  Score 2439;  DB 4;  Length 1713;
  Best Local Similarity   81.9%;  Pred. No. 1.4e-234;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQPAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::||||||||||||||||:|||||  |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQPARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :||||||||||: |||||||||||:|||||  ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||:|||||||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:|||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 7
US-09-538-092-1359
; Sequence 1359, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1359
;   LENGTH: 1713
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number Q16787
US-09-538-092-1359

  Query Match             83.0%;  Score 2439;  DB 4;  Length 1713;
  Best Local Similarity   81.9%;  Pred. No. 1.4e-234;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQPAKLNYTKEATSN 120
              ||||||||||||||||||:|:||:||:||::||||||||||||||||:|||||  |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQPARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :||||||||||: |||||||||||:|||||  ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | |||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:|||||||||||||||||||||:|||||||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:|||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 8
PCT-US94-10261A-24
; Sequence 24, Application PC/TUS9410261A
;  GENERAL INFORMATION:
;    APPLICANT:  Carter, William G.
;    APPLICANT:  Gil, Susanna A.
;    APPLICANT:  Ryan, Maureen C.
;    TITLE OF INVENTION:  Epiligrin, an Epithelial Ligand for
;    TITLE OF INVENTION:  Integrins
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen, O'Connor, Johnson, and Kindness
```

```
;       STREET:  1420 Fifth Avenue
;       CITY:  Seattle
;       STATE:  WA
;       COUNTRY:  USA
;       ZIP:  98101-8100
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/10261A
;       FILING DATE:  02-SEP-1994
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Shelton, Dennis K.
;       REGISTRATION NUMBER:  26,997
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 682-8100
;       TELEFAX:  (206) 224-0779
;   INFORMATION FOR SEQ ID NO:  24:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1713 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;       DESCRIPTION:  E170 protein as translated from sequence of
;       DESCRIPTION:  FIGURES 15A-15F, and as shown also in FIGURES 19A-19R
PCT-US94-10261A-24

  Query Match           83.0%;  Score 2439;  DB 5;  Length 1713;
  Best Local Similarity  81.9%;  Pred. No. 1.4e-234;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        771 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 830

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              |||||||||||||||||||:|:||:||::||||||||||||||||:||||| |||:
Db        831 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 890

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: |||||||||||:||||| ||||||||||||||||
Db        891 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 950

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        951 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1010

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1011 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1070

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||:|||||||||||||||||||
Db       1071 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1130

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:|||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1131 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1190

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1191 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1250

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1251 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1310

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1311 KPPFLMLLKGSTRFNKTKTFRINQL 1335
```

```
RESULT 9
US-09-560-385A-2
; Sequence 2, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
;  APPLICANT:  Boutand, Ariel
;  TITLE OF INVENTION:  Recombinant Laminin 5
;  FILE REFERENCE:  99-274-C
;  CURRENT APPLICATION NUMBER: US/09/560,385A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1724
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-560-385A-2

  Query Match           83.0%;  Score 2439;  DB 4;  Length 1724;
  Best Local Similarity  81.9%;  Pred. No. 1.4e-234;
  Matches  463;  Conservative   47;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||: |||||||:||||||||||||:||||
Db        782 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRENGGTENMFVMYLGNKDASRDYIG 841

Qy         61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKEATSN 120
              |||||||||||||||||||:|:||:||::||||||||||||||||:||||| |||:
Db        842 MAVVDGQLTCVYNLGDREAELQVDQILTKSETKEAVMDRVKFQRIYQFARLNYTKGATSS 901

Qy        121 KPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDDLNEN 180
              ||: | |||::| :|||||||||: |||||||||||:||||| ||||||||||||||||
Db        902 KPETPGVYDMDGRNSNTLLNLDPENVVFYVGGYPPDFKLPSRLSFPPYKGCIELDDLNEN 961

Qy        181 VLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTTV 240
              |||||||| ||||||||||||||||||||||||||||:||||:|| | | |||||||
Db        962 VLSLYNFKKTFNLNTTEVEPCRRRKEESDKNYFEGTGYARVPTQPHAPIPTFGQTIQTTV 1021

Qy        241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIRDTINDGKDHSILITIGKLQ 300
              |||||||||| | ||||||||| |||||||||| |||:|: | ||:|:|||| | |||||
Db       1022 DRGLLFFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDAINNGRDHSIQIKIGKLQ 1081

Qy        301 KRMWINVNERSVRIEGEIFDFSTYYLGGIPIAIRERFNISTPAFQGCMKNLKKTSGVVRL 360
              |||||||: ::  |:||:||||||||||||||||||||||:|||||||||||||||||||
Db       1082 KRMWINVDVQNTIIDGEVFDFSTYYLGGIPIAIRERFNISTPAFRGCMKNLKKTSGVVRL 1141

Qy        361 NDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQ 420
              |||||||||||||||||:|||||||:|||:| :| ||  | ||||||||||| ||:||
Db       1142 NDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQ 1201

Qy        421 TRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLR 480
              | | :| ||||||:||||| ||  |||||| ||||||||:|||||| ||||||||||:||
Db       1202 TWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLR 1261

Qy        481 RNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 540
               ::||   |:::|||||| :|||||||| ||| | ||||||| | | |:| ||||||||
Db       1262 NSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLN 1321

Qy        541 KPPFLMLFKSPKRFNKGRIFNVNQL 565
              ||||||| |   |||| : | :|||
Db       1322 KPPFLMLLKGSTRFNKTKTFRINQL 1346


RESULT 10
US-08-445-135-2
; Sequence 2, Application US/08445135
; Patent No. 5658789
;  GENERAL INFORMATION:
;    APPLICANT:  Quaranta, Vito
;    APPLICANT:  Hormia, Marketta
;    TITLE OF INVENTION:  Promotion of Epithelial Cell Adhesion
```

```
;    TITLE OF INVENTION:  and Hemidesmosome Assembly by a Laminin-Like Molecule
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson and Bear
;      STREET:  620 Newport Center Drive, Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/445,135
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/151,134
;      FILING DATE:  12-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Israelsen, Ned A.
;      REGISTRATION NUMBER:  29,655
;      REFERENCE/DOCKET NUMBER:  DESMOS.002CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 235-8550
;      TELEFAX:  (619) 235-0176
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  770 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    IMMEDIATE SOURCE:
;      CLONE:  150 kD
US-08-445-135-2

  Query Match             44.6%;  Score 1310;  DB 1;  Length 770;
  Best Local Similarity   90.9%;  Pred. No. 5.7e-122;
  Matches  259;  Conservative    3;  Mismatches   13;  Indels   10;  Gaps    4;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 550

Qy         61 MA----VVDGQLTCVYNLGDREAEVQIDQV-LTESESQEAVMDRVKFQRIYQFAKLNYTK 115
              :       |    |:   | |    | |:  ||||||||||||||||||||||||||||
Db        551 IGGCRWPAD---VCLQPGGPR--SVSSDRSGLTESESQEAVMDRVKFQRIYQFAKLNYTK 605

Qy        116 EATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELD 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 EATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELD 665

Qy        176 DLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQT 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 DLNENVLSLYNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGYARIPTQPNAPFPNFIQT 725

Qy        236 IQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGI 280
              ||||| ||||||||||||||||||||||||||||||||||||||
Db        726 IQTTVARGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGI 770


RESULT 11
US-09-949-016-10932
; Sequence 10932, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10932
;   LENGTH: 3647
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10932

  Query Match             24.3%;  Score 715;  DB 4;  Length 3647;
  Best Local Similarity   33.1%;  Pred. No. 3.5e-61;
  Matches  194;  Conservative   96;  Mismatches  214;  Indels   82;  Gaps   21;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMYLGNKDASKDYIG 60
              |:|||:|||::| | || ||  ||:|  :|| |:     |||| ||||:|:: |: ||:|
Db       2700 MKFNGRSGVQLRTPRDLADLAAYTALKFYLQGPEPEPGQGTEDRFVMYMGSRQATGDYMG 2759

Qy         61 MAVVDGQLTCVYNLGDR-EAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE--- 116
              ::: | ::  || ||:   | : ||: : |          |   |  ||  :: | |
Db       2760 VSLRDKKVHWVYQLGEAGPAVLSIDEDIGEQ------FAAVSLDRTLQFGHMSVTVERQM 2813

Qy        117 --ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIEL 174
                |      ||     ||      |||| |:| |||||||||  |  |  |||| |:||||:
Db       2814 IQETKGDTVAPGA---EG-----LLNLRPDDFVFYVGGYPSTFTPPPLLRFPGYRGCIEM 2865

Qy        175 DDLNENVLSLYNFKTTFNLNTTEVEPCRRRKEE-----SDKNYFEGTGYARIPTQPN-AP 228
              | ||| |:|||||: || |:|     || | |        :| :| :|||:|||      :
Db       2866 DTLNEEVVSLYNFERTFQLDTAVDRPCARSKSTGDPWLTDGSYLDGTGFARISFDSQIST 2925

Qy        229 FPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRYKLNS--------EPP----- 275
              | | ::     |:||| : |   |: | :::|:|:: |   :         :||
Db       2926 TKRFEQELRLVSYSGVLFFLKQQSQFLCLAVQEGSLVLLYDFGAGLKKAVPLQPPPPLTS 2985

Qy        276 KEKGIRDTINDGKDHSILITIGKLQKRMWINVNER---SVRIEGEIFDFSTYYLGGI--- 329
              | |:           :  :|  :||: : |       ||  : ::     |||||:
Db       2986 ASKAIQ----------VFLLGGSRKRVLVRVERATVYSVEQDNDLELADAYYLGGVPPD 3034

Qy        330 --PIAIRERFNISTPAFQGCMKNLK---KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSR 384
              | ::|  |  :  : :||:| :|    |   : ||| | ||:  |: |  : |  :|
Db       3035 QLPPSLRRLFP-TGGSVRGCVKGIKALGKYVDLKRLN-TTGVSAGCTADLLVGRAMTFHG 3092

Qy        385 GG--QMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDS 442
              |  ::: :|:  | |       ||| : | |  |     :      |:|: | : |    :
Db       3093 HGFLRLALSNV-APLTGNVYSGFGFHSAQDSALLYYRASPDGLCQVSLQQGRVSLQLLRT 3151

Qy        443 NIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQV--LRRNQRLPSFSNAQQS----LR 496
              :  |:  : ||  |:|:  |: :|: | :|||:  :: ::  |      |       |
Db       3152 EV---KTQAGFADGAPHYVAFYSNATGVWLYVDDQLQQMKPHRGPPPELQPQPEGPPRLL 3208

Qy        497 LGG-------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLG 535
              |||        :| |||||| |||       | ||      : | |
Db       3209 LGGLPESGTIYNFSGCISNVFVQRLLGPQRVFDLQQNLGSVNVSTG 3254


RESULT 12
US-09-561-818A-4
; Sequence 4, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
;  APPLICANT: Kortesmaa, Jarrko
;  APPLICANT:  Tryggvason, Karl
;  TITLE OF INVENTION: Laminin 8 and Methods For Its Use
;  FILE REFERENCE: 99,274-D
```

```
;  CURRENT APPLICATION NUMBER: US/09/561,818A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1792
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-561-818A-4

  Query Match             23.6%;  Score 694;  DB 4;  Length 1792;
  Best Local Similarity   32.1%;  Pred. No. 1.3e-59;
  Matches  193;  Conservative  101;  Mismatches  246;  Indels   62;  Gaps   20;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFL----QRPDLRENGGTEDMFVMYLGNKDASK 56
              | |:|:| |||      ::||| :|||||::    :||:| |    | | |::|||:|:| |
Db        805 MMFDGQSAVEVHSRTSMDDLKAFTSLSLYMKPPVKRPELTE---TADQFILYLGSKNAKK 861

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
              :|:|:|: :  |  ||||| :: |: :|       |  |     || :|: :  |:  |
Db        862 EYMGLAIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVP 919

Qy        117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDD 176
              : |:  :   :   |    ::||:|||| |||||| | :|:||: |  | : ||:||
Db        920 SLSSTAEEKFIKKGEFSGDDSLLDLDPEDTVFYVGGVPSNFKLPTSLNLPGFVGCLELAT 979

Qy        177 LNENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYARIPTQPN----A 227
              || :|:|||||  :|:: :   || | |       :  :|:|:||| :   |
Db        980 LNNDVISLYNFKHIYNMDPSTSVPCARDKLAFTQSRAASYFFDGSGYAVVRDIPRRGKFG 1039

Qy        228 PFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRY-------KLNSEPPKEKGI 280
                |   ::|  | ||:    |   | : :| | | |       ::: |   :|
Db       1040 QVTRFDIEVRTPADNGLILLMVNGSMFFRLEMRNGYLHVFYDFGFSSGRVHLEDTLKKA- 1098

Qy        281 RDTINDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIP------I 331
                ||| | | | | |    |:| : |: | |:     |      |:  |:|| |
Db       1099 --QINDAKYHEISI-IYHNDKKMILVVDRRHVKSMDNEKMKIPFTDIYIGGAPPEILQSR 1155

Qy        332 AIRERFNISTPAFQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQM 388
              |:|    :    |:|||     ||   ::   :|:||   | ||  : | | |:  ||
Db       1156 ALRAHLPLDI-NFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQS 1212

Qy        389 SFTNLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIF 447
              ::  :   | |:  | |:| ||:| |  : : :    ::|::| : :  :   | :
Db       1213 FIASIQKISFFDGFEGGFNFRTLQPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQ 1270

Qy        448 KSPGTYMDGLLHHVSVISDTSGLR--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-- 499
                | ||| |   |||  |  |  |::|  :|  :|          | | :    ||
Db       1271 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSP 1328

Qy        500 -----GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
                  :| |||||    |  :  || |    : |   ||  | :  |  :| |  |
Db       1329 ISAQYANFTGCISNAYFTRVDRDVEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNL 1388

Qy        555 NK 556
              :|
Db       1389 SK 1390


RESULT 13
US-09-561-818A-8
; Sequence 8, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
;  APPLICANT: Kortesmaa, Jarrko
;  APPLICANT:  Tryggvason, Karl
;  TITLE OF INVENTION: Laminin 8 and Methods For Its Use
;  FILE REFERENCE: 99,274-D
;  CURRENT APPLICATION NUMBER: US/09/561,818A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 1800
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-561-818A-8

  Query Match             23.6%;  Score 694;  DB 4;  Length 1800;
  Best Local Similarity   32.1%;  Pred. No. 1.4e-59;
  Matches  193;  Conservative  101;  Mismatches  246;  Indels   62;  Gaps   20;

Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFL----QRPDLRENGGTEDMFVMYLGNKDASK 56
              | |:|:| |||      ::||| :|||||::    :||:| |    | | |::|||:|:| |
Db        805 MMFDGQSAVEVHSRTSMDDLKAFTSLSLYMKPPVKRPELTE---TADQFILYLGSKNAKK 861

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
              :|:|:|: :  |  ||||| :: |: :|       |  |     || :|: :  |:  |
Db        862 EYMGLAIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVP 919

Qy        117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDD 176
              : |:  :   :   |    ::||:|||| |||||| | :|:||: |  | : ||:||
Db        920 SLSSTAEEKFIKKGEFSGDDSLLDLDPEDTVFYVGGVPSNFKLPTSLNLPGFVGCLELAT 979

Qy        177 LNENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYARIPTQPN----A 227
              || :|:|||||  :|:: :   || | |       :  :|:|:||| :   |
Db        980 LNNDVISLYNFKHIYNMDPSTSVPCARDKLAFTQSRAASYFFDGSGYAVVRDIPRRGKFG 1039

Qy        228 PFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRY-------KLNSEPPKEKGI 280
                |   ::|  | ||:    |   | : :| | | |       ::: |   :|
Db       1040 QVTRFDIEVRTPADNGLILLMVNGSMFFRLEMRNGYLHVFYDFGFSSGRVHLEDTLKKA- 1098

Qy        281 RDTINDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIP------I 331
                ||| | | | | |    |:| : |: | |:     |      |:  |:|| |
Db       1099 --QINDAKYHEISI-IYHNDKKMILVVDRRHVKSMDNEKMKIPFTDIYIGGAPPEILQSR 1155

Qy        332 AIRERFNISTPAFQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQM 388
              |:|    :    |:|||     ||   ::   :|:||   | ||  : | | |:  ||
Db       1156 ALRAHLPLDI-NFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQS 1212

Qy        389 SFTNLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIF 447
              ::  :   | |:  | |:| ||:| |  : : :    ::|::| : :  :   | :
Db       1213 FIASIQKISFFDGFEGGFNFRTLQPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQ 1270

Qy        448 KSPGTYMDGLLHHVSVISDTSGLR--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-- 499
                | ||| |   |||  |  |  |::|  :|  :|          | | :    ||
Db       1271 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSP 1328

Qy        500 -----GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
                  :| |||||    |  :  || |    : |   ||  | :  |  :| |  |
Db       1329 ISAQYANFTGCISNAYFTRVDRDVEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNL 1388

Qy        555 NK 556
              :|
Db       1389 SK 1390


RESULT 14
US-09-561-818A-2
; Sequence 2, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
;  APPLICANT: Kortesmaa, Jarrko
;  APPLICANT:  Tryggvason, Karl
;  TITLE OF INVENTION: Laminin 8 and Methods For Its Use
;  FILE REFERENCE: 99,274-D
;  CURRENT APPLICATION NUMBER: US/09/561,818A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1816
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-561-818A-2
```

Query Match 23.6%; Score 694; DB 4; Length 1816;
Best Local Similarity 32.1%; Pred. No. 1.4e-59;
Matches 193; Conservative 101; Mismatches 246; Indels 62; Gaps 20;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFL----QRPDLRENGGTEDMFVMYLGNKDASK 56
              | |:|:| |||     ::||| :|||||::    :||:| |   | | |::|||:|:| |
Db        829 MMFDGQSAVEVHSRTSMDDLKAFTSLSLYMKPPVKRPELTE---TADQFILYLGSKNAKK 885

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
              :|:|:|: :  |  ||||| :: |: :|       |  |    || :|: :  |:  |
Db        886 EYMGLAIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVP 943

Qy        117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDD 176
              : |:  :   :   |    ::||:|||| |||||| | :|:||: |  | : ||:||
Db        944 SLSSTAEEKFIKKGEFSGDDSLLDLDPEDTVFYVGGVPSNFKLPTSLNLPGFVGCLELAT 1003

Qy        177 LNENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYARIPTQPN----A 227
              || :|:|||||  :|:: :   || | |       :  :|:|:||| :   |
Db       1004 LNNDVISLYNFKHIYNMDPSTSVPCARDKLAFTQSRAASYFFDGSGYAVVRDIPRRGKFG 1063

Qy        228 PFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRY-------KLNSEPPKEKGI 280
              |   ::|  | ||:    |   |  | : :| | | |       ::: |   :|
Db       1064 QVTRFDIEVRTPADNGLILLMVNGSMFFRLEMRNGYLHVFYDFGFSSGRVHLEDTLKKA- 1122

Qy        281 RDTINDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIP------I 331
              ||| | | | | |    |:| : |: | |:    |      |:  |:|| |
Db       1123 --QINDAKYHEISI-IYHNDKKMILVVDRRHVKSMDNEKMKIPFTDIYIGGAPPEILQSR 1179

Qy        332 AIRERFNISTPAFQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQM 388
              |:|    :    |:|||      ||   ::   :|:||   | ||  : | | |:  ||
Db       1180 ALRAHLPLDI-NFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQS 1236

Qy        389 SFTNLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIF 447
              ::  :   | |:  | |:| ||:| |  : : :    ::|::| : :  :   | :
Db       1237 FIASIQKISFFDGFEGGFNFRTLQPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQ 1294

Qy        448 KSPGTYMDGLLHHVSVISDTSGLR--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-- 499
              | ||| |   ||| |  |  |::|  :|  :|         | | :    ||
Db       1295 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSP 1352

Qy        500 -----GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
                 :| |||||    |  :  || |    : |   ||  | :   |  :| | |
Db       1353 ISAQYANFTGCISNAYFTRVDRDVEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNL 1412

Qy        555 NK 556
              :|
Db       1413 SK 1414
```

RESULT 15
US-09-561-818A-6
; Sequence 6, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortesmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1824
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-6

Query Match 23.6%; Score 694; DB 4; Length 1824;
Best Local Similarity 32.1%; Pred. No. 1.4e-59;
Matches 193; Conservative 101; Mismatches 246; Indels 62; Gaps 20;

```
Qy          1 MRFNGKSGVEVRLPNDLEDLKGYTSLSLFL----QRPDLRENGGTEDMFVMYLGNKDASK 56
              | |:|:| |||     ::||| :|||||::    :||:| |   | | |::|||:|:| |
Db        829 MMFDGQSAVEVHSRTSMDDLKAFTSLSLYMKPPVKRPELTE---TADQFILYLGSKNAKK 885

Qy         57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTESESQEAVMDRVKFQRIYQFAKLNYTKE 116
              :|:|:|: :  |  ||||| :: |: :|       |  |    || :|: :  |:  |
Db        886 EYMGLAIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAYFSIVKIERVGKHGKVFLTVP 943

Qy        117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYVGGYPPDFELPSRLRFPPYKGCIELDD 176
              : |:  :   :   |    ::||:|||| |||||| | :|:||: |  | : ||:||
Db        944 SLSSTAEEKFIKKGEFSGDDSLLDLDPEDTVFYVGGVPSNFKLPTSLNLPGFVGCLELAT 1003

Qy        177 LNENVLSLYNFKTTFNLNTTEVEPCRRRK-----EESDKNYFEGTGYARIPTQPN----A 227
              || :|:|||||  :|:: :   || | |       :  :|:|:||| :   |
Db       1004 LNNDVISLYNFKHIYNMDPSTSVPCARDKLAFTQSRAASYFFDGSGYAVVRDIPRRGKFG 1063

Qy        228 PFPNFIQTIQTTVDRGLLFFAENQDNFISLNIEDGNLMVRY-------KLNSEPPKEKGI 280
              |   ::|  | ||:    |   |  | : :| | | |       ::: |   :|
Db       1064 QVTRFDIEVRTPADNGLILLMVNGSMFFRLEMRNGYLHVFYDFGFSSGRVHLEDTLKKA- 1122

Qy        281 RDTINDGKDHSILITIGKLQKRMWINVNERSVRI---EGEIFDFSTYYLGGIP------I 331
              ||| | | | | |    |:| : |: | |:    |      |:  |:|| |
Db       1123 --QINDAKYHEISI-IYHNDKKMILVVDRRHVKSMDNEKMKIPFTDIYIGGAPPEILQSR 1179

Qy        332 AIRERFNISTPAFQGCMKNL---KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQM 388
              |:|    :    |:|||      ||   ::   :|:||   | ||  : | | |:  ||
Db       1180 ALRAHLPLDI-NFRGCMKGFQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQS 1236

Qy        389 SFTNLD-VPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIF 447
              ::  :   | |:  | |:| ||:| |  : : :    ::|::| : :  :   | :
Db       1237 FIASIQKISFFDGFEGGFNFRTLQPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQ 1294

Qy        448 KSPGTYMDGLLHHVSVISDTSGLR--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-- 499
              | ||| |   ||| |  |  |::|  :|  :|         | | :    ||
Db       1295 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSP 1352

Qy        500 -----GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRF 554
                 :| |||||    |  :  || |    : |   ||  | :   |  :| | |
Db       1353 ISAQYANFTGCISNAYFTRVDRDVEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNL 1412

Qy        555 NK 556
              :|
Db       1413 SK 1414
```

Search completed: February 22, 2005, 08:40:55
Job time : 29.3827 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:05:49 ; Search time 5.81686 Seconds
(without alignments)
3605.942 Million cell updates/sec

Title: US-10-817-423-6
Perfect score: 1118
Sequence: 1 MKNLKKTSGVVRLNDTVGVT.....MLFKSPKRFNKGRIFNVNQL 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	850	76.0	1713	2	A55347	adhesive ligand ep
2	187	16.7	1816	1	S68960	laminin alpha-4 ch
3	186	16.6	3635	2	T10053	laminin alpha 5 ch
4	173.5	15.5	3712	2	S18253	laminin alpha-1 ch
5	144.5	12.9	3106	1	S53868	laminin alpha-2 ch
6	134.5	12.0	1751	1	MMHUMH	laminin alpha-2 ch
7	115.5	10.3	3102	2	T43291	laminin alpha chai
8	111.5	10.0	3084	1	MMMSA	laminin alpha-1 ch
9	107	9.6	3097	2	T00021	DN-cadherin - frui
10	105	9.4	5147	1	IJFFTM	cadherin-related t
11	101.5	9.1	3075	2	S14458	laminin alpha-1 ch
12	99.5	8.9	3672	2	T23433	hypothetical prote
13	99.5	8.9	3704	2	T37316	probable laminin a
14	99	8.9	1158	2	E86327	protein F18O14.19
15	94.5	8.5	675	1	KXBOS	plasma protein S p
16	94	8.4	1722	2	E89753	protein F11C7.4 [i
17	92.5	8.3	487	2	PQ0259	hypothetical prote
18	91.5	8.2	403	2	A26371	sex steroid-bindin
19	91.5	8.2	714	2	S68603	hypothetical prote
20	91.5	8.2	882	2	A39030	androgen-binding p
21	91	8.1	206	2	F84459	hypothetical prote
22	91	8.1	510	1	S56640	ferredoxin-nitrite
23	91	8.1	729	2	F86308	Similar to disease
24	91	8.1	2823	2	F87908	protein T22A3.8 [i
25	91	8.1	2823	2	T23064	hypothetical prote
26	91	8.1	4351	2	T00252	MEGF1 protein - ra
27	90.5	8.1	2325	2	A61208	chondroitin sulfat
28	89.5	8.0	272	2	T30305	dnaA protein - Lac
29	89.5	8.0	1381	2	T31083	paranodin - rat
30	88	7.9	1264	2	T19545	hypothetical prote
31	87.5	7.8	1283	2	T13799	neurexin IV - frui
32	86.5	7.7	642	2	S53433	plasma protein S p
33	86.5	7.7	1531	2	T42218	slit-1 protein hom
34	85.5	7.6	935	2	A64608	excinuclease ABC c
35	84.5	7.6	776	2	T19900	hypothetical prote
36	84.5	7.6	1385	2	T14158	neurexin IV - mous
37	84	7.5	629	2	S63369	hypothetical prote
38	82.5	7.4	307	2	D90394	purine nucleosidas
39	82.5	7.4	468	2	B40228	neurexin I-beta pr
40	82.5	7.4	1530	2	I45944	neurexin I-alpha -
41	82	7.3	428	1	E69044	diaminopimelate de
42	81.5	7.3	336	2	T27762	hypothetical prote
43	81.5	7.3	446	2	D64210	replicative DNA he
44	81.5	7.3	1365	2	A41483	glucosyltransferas
45	81.5	7.3	1507	2	A40228	neurexin I-alpha p

ALIGNMENTS

RESULT 1
A55347
adhesive ligand epiligrin, alpha-3 chain form A precursor - human
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C;Accession: A55347
R;Ryan, M.C.; Tizard, R.; VanDevanter, D.R.; Carter, W.G.
J. Biol. Chem. 269, 22779-22787, 1994
A;Title: Cloning of the LamA3 gene encoding the alpha3 chain of the adhesive ligand epi
A;Reference number: A55347; MUID:94357926; PMID:8077230
A;Accession: A55347
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1713 <RYA>
A;Cross-references: UNIPROT:Q16787; GB:L34155; NID:g551596; PID:g551597
C;Superfamily: laminin alpha-4 chain; laminin G repeat homology; laminin-type EGF-like
C;Keywords: alternative splicing
F;67-114/Domain: laminin-type EGF-like homology <LE2>
F;1392-1534/Domain: laminin G repeat homology <LG4>

Query Match 76.0%; Score 850; DB 2; Length 1713;
Best Local Similarity 76.6%; Pred. No. 1.1e-69;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

```
Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1118 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1177

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| ||||||:||||| ||  |||||| |||||||:||||||
Db       1178 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1237

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              |||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1238 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1297

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
               |:| |||||||||||||| |   |||| : | :|||
Db       1298 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1335
```

RESULT 2
S68960
laminin alpha-4 chain precursor - human
N;Alternate names: laminin Ah
C;Species: Homo sapiens (man)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: S68960; S65926; S49149; S40150; I53516
R;Richards, A.; Al-Imara, L.; Pope, F.M.
Eur. J. Biochem. 238, 813-821, 1996
A;Title: The complete cDNA sequence of laminin alpha-4 and its relationship to the othe
A;Reference number: S68960; MUID:96300249; PMID:8706685

A;Accession: S68960
A;Molecule type: mRNA
A;Residues: 1-1816 <RIC>
A;Cross-references: UNIPROT:Q16363; UNIPROT:Q14731; EMBL:X91171; NID:g1212962; PIDN:CAA6
A;Experimental source: tissue type heart
R;Iivanainen, A.; Sainio, K.; Sariola, H.; Tryggvason, K.
FEBS Lett. 365, 183-188, 1995
A;Title: Primary structure and expression of a novel human laminin alpha-4 chain.
A;Reference number: I53516; MUID:95300971; PMID:7781776
A;Accession: S65926
A;Molecule type: mRNA
A;Residues: 1-142,'P',144-177,'F',179-490,'Y',492-1056,'P',1058-1816 <IIV>
A;Cross-references: EMBL:S78569; NID:g1042081; PIDN:AAB34635.1; PID:g1042082
R;Richards, A.J.; Al-Imara, L.; Carter, N.; Leversha, M.; Lloyd, J.C.; Pope, F.M.
submitted to the EMBL Data Library, December 1993
A;Description: Localisation of the gene (LAMA4) to chromosome 6q21 and isolation of a pa
A;Reference number: S49149
A;Accession: S49149
A;Molecule type: mRNA
A;Residues: 236-1816 <RI2>
A;Cross-references: EMBL:X76939; NID:g509805; PIDN:CAA54258.1; PID:g509806
R;Richards, A.J.; Al-Imara, L.; Carter, N.; Lloyd, J.C.; Pope, F.M.
submitted to the EMBL Data Library, February 1993
A;Description: Isolation of a partial cDNA encoding a protein homologous to laminin A. A
A;Reference number: S40150
A;Accession: S40150
A;Molecule type: mRNA
A;Residues: 1403-1541,'S',1543-1816 <RI3>
A;Cross-references: EMBL:X70904; NID:g437804; PIDN:CAA50261.1; PID:g437805
C;Genetics:
A;Gene: GDB:LAMA4; LAMA3
A;Cross-references: GDB:203904; OMIM:600133
A;Map position: 6q21-6q21
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin alpha-4 chain; laminin G repeat homology; laminin-type EGF-like h
C;Keywords: basement membrane; cell binding; coiled coil; extracellular matrix; glycoprc
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-1816/Product: laminin alpha-4 chain #status predicted <MAT>
F;82-129/Domain: laminin-type EGF-like homology <LE1>
F;132-184/Domain: laminin-type EGF-like homology <LE2>
F;187-238/Domain: laminin-type EGF-like homology <LE3>
F;241-265/Domain: laminin-type EGF-like homology #status atypical <LE4>
F;717-719/Region: cell attachment (R-G-D) motif
F;862-1031/Domain: laminin G repeat homology <LG1>
F;1068-1223/Domain: laminin G repeat homology <LG2>
F;1252-1398/Domain: laminin G repeat homology <LG3>
F;1488-1636/Domain: laminin G repeat homology <LG4>
F;1665-1816/Domain: laminin G repeat homology <LG5>
F;104,215,308,458,524,550,571,574,631,639,735,751,754,780,803,1086,1281,1359,1411/Bindin
F;266,269/Disulfide bonds: interchain #status predicted

Query Match 16.7%; Score 187; DB 1; Length 1816;
Best Local Similarity 28.3%; Pred. No. 1.6e-08;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

```
Qy          5 KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD-VPSTDRFQLSFGFQTF 63
              ||   ::   :|:||   | ||  : | | |:  ||    ::  :   | |:  | |:|
Db       1202 KKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIASIQKISFFDGFEGGFNFRTL 1259

Qy         64 QPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGL 123
              ||:| |  : : :    ::|::| : :  :   | :      | ||| |   |||  |
Db       1260 QPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQSVDKQYNDGLSHF--VISSVSPT 1315

Qy        124 R--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-------GHFEGCISNVLVQRFSQS 170
              |  |::|  :|  :|       | | :   ||        :| |||||    |  :
Db       1316 RYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSPISAQYANFTGCISNAYFTRVDRD 1375

Qy        171 PEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 209
              || |    : |   ||  | :   | :| |  |  :|
Db       1376 VEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNLSK 1414
```

RESULT 3
T10053
laminin alpha 5 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10053
R;Miner, J.H.; Lewis, R.M.; Sanes, J.R.
submitted to the EMBL Data Library, November 1997
A;Reference number: Z16923
A;Accession: T10053
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3635 <MIN>
A;Cross-references: UNIPROT:Q61001; EMBL:U37501; NID:g2599231; PID:g2599232
C;Genetics:
A;Gene: Lama5
C;Keywords: basement membrane; cell binding; extracellular matrix
F;1888-1939/Domain: laminin-type EGF-like homology <LEG>
F;1942-1970/Domain: EGF homology <EGF>

Query Match 16.6%; Score 186; DB 2; Length 3635;
Best Local Similarity 29.2%; Pred. No. 5.2e-08;
Matches 59; Conservative 34; Mismatches 91; Indels 18; Gaps 6;

```
Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDV-PSTDRFQLSFG 59
              :| | |   : ||| | |::  |: |  : || :|   | :     || | |:     ||
Db       3015 IKALGKYVDLKRLN-TTGISFGCTADLLVGRTMTFHGHGFLPLALPDVAPITEVVYSGFG 3073

Qy         60 FQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISD 119
              |:  | :  |    :       |:| :|: |   :  :   ::   : ||  |:|:  |:
Db       3074 FRGTQDNNLLYYRTSPDGPYQVSLREGHVTLRFMNQEV---ETQRVFADGAPHYVAFYSN 3130

Qy        120 TSGLRLLIDD--QVLRRNQRLPSFSNAQ----QSLRLGG-------GHFEGCISNVLVQR 166
              :|: | :||  |::: ::|       |       | |||         :| |||||| |||
Db       3131 VTGVWLYVDDQLQLVKSHERTTPMLQLQPEEPSRLLLGGLPVSGTFHNFSGCISNVFVQR 3190

Qy        167 FSQSPEVLDLASKSTKKDASLG 188
                 | ||       : |:|
Db       3191 LRGPQRVFDLHQNMGSVNVSVG 3212
```

RESULT 4
S18253
laminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C;Accession: S28399; S18253
R;Kusche-Gullberg, M.; Garrison, K.; MacKrell, A.J.; Fessler, L.I.; Fessler, J.H.
EMBO J. 11, 4519-4527, 1992
A;Title: Laminin A chain: expression during Drosophila development and genomic sequence
A;Reference number: S28399; MUID:93049203; PMID:1425586
A;Accession: S28399
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-3712 <KUS>
A;Cross-references: UNIPROT:Q00174; GB:M96388; NID:g157799; PIDN:AAA28662.1; PID:g157800
R;Garrison, K.; MacKrell, A.J.; Fessler, J.H.
J. Biol. Chem. 266, 22899-22904, 1991
A;Title: Drosophila laminin A chain sequence, interspecies comparison, and domain struct
A;Reference number: S18253; MUID:92078147; PMID:1744083
A;Accession: S18253
A;Molecule type: mRNA
A;Residues: 1762-3712 <GAR>
A;Cross-references: EMBL:M75882; NID:g157797; PIDN:AAA28661.1; PID:g157798
C;Genetics:
A;Gene: FlyBase:LanA
A;Cross-references: FlyBase:FBgn0002526
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C;Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular
F;273-330/Domain: laminin-type EGF-like homology <LEG>
F;333-400/Domain: laminin-type EGF-like homology <LE02>
F;541-584/Domain: laminin-type EGF-like homology <LEG1>

```
F;1776-2115/Domain: III <DOM3>
F;1776-1806/Domain: laminin-type EGF-like homology #status atypical <LE1>
F;1809-1856/Domain: laminin-type EGF-like homology <LE2>
F;1859-1914/Domain: laminin-type EGF-like homology <LE3>
F;1917-1967/Domain: laminin-type EGF-like homology <LE4>
F;1970-2014/Domain: laminin-type EGF-like homology <LE5>
F;2017-2061/Domain: laminin-type EGF-like homology <LE6>
F;2064-2109/Domain: laminin-type EGF-like homology <LE7>
F;2116-2697/Domain: I/II, heptad repeats <DOM2>
F;2698-3712/Domain: G <DOMG>
F;2698-2863/Domain: repeat G1 <RG1>
F;2864-3048/Domain: repeat G2 <RG2>
F;3049-3223/Domain: repeat G3 <RG3>
F;3079-3200/Domain: laminin G repeat homology <LG3>
F;3334-3528/Domain: repeat G4 <RG4>
F;3529-3712/Domain: repeat G5 <RG5>
F;1847,1850,1943,2024,2196,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2890,2938,3

  Query Match             15.5%;  Score 173.5;  DB 2;  Length 3712;
  Best Local Similarity   27.9%;  Pred. No. 7.6e-07;
  Matches   65;  Conservative   43;  Mismatches   66;  Indels   59;  Gaps   12;

Qy          3 NLKKTSGVVRLNDTV---GVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFG 59
              |:    ||| | : |   || : ||  :  | : :    | :   |  | |  :   :
Db       3025 NVVINQGVVDLTEYVTGGGVEEGCSAKFSTVVSYAPHEYGFLRMNN--VSSDNNLHVVLH 3082

Qy         60 FQTPQPSGTLL---NHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLH---- 112
              |:| ||:| |    ||  ::|:: ::|:|| ::|::  | : |         | :|:
Db       3083 FKTTQPNGVLFYAANHD-QSSTIGLSLQDGLLKLNSMGSQLVI-------DDRILNDGED 3134

Qy        113 HVSVISDTSG-LRLLIDDQVLRRNQRLPSFSNAQQSLRLGGG------------------ 153
              ||  :  | | ||| :||     |:|| |      | | | ||
Db       3135 HVVTVQHTQGELRLTVDDV---DNKRLGS----PQPLILEGGDIFFAGLPDNYRTPRNAL 3187

Qy        154 ----HFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFK 202
                 :| ||||:| |     : |::: |: : ||: :: ||    || :: ::
Db       3188 ASLAYFVGCISDVTV-----NEEIINFANSAEKKNGNINGC----PPHVLAYE 3231


RESULT 5
S53868
laminin alpha-2 chain precursor - mouse
N;Alternate names: laminin M chain; merosin heavy chain
C;Species: Mus musculus (house mouse)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: I49077; S50829; I48655; S31576; S53868
R;Bernier, S.M.; Utani, A.; Sugiyama, S.; Doi, T.; Polistina, C.; Yamada, Y.
Matrix Biol. 14, 447-455, 1995
A;Title: Cloning and expression of laminin alpha 2 chain (M-chain) in the mouse.
A;Reference number: I49077; MUID:95316259; PMID:7795883
A;Accession: I49077
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3106 <RES>
A;Cross-references: UNIPROT:Q60675; EMBL:U12147; NID:g699109; PIDN:AAC52165.1; PID:g6991
R;Xu, H.; Wu, X.R.; Wewer, U.M.; Engvall, E.
Nature Genet. 8, 297-302, 1994
A;Title: Murine muscular dystrophy caused by a mutation in the laminin alpha-2 (Lama2) g
A;Reference number: S50829; MUID:95179178; PMID:7874173
A;Accession: S50829
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 64-281 <XUH>
A;Cross-references: GB:S75315; NID:g833929; PIDN:AAB33573.1; PID:g833930
R;Chang, A.C.; Wadsworth, S.; Coligan, J.E.
J. Immunol. 151, 1789-1801, 1993
A;Title: Expression of merosin in the thymus and its interaction with thymocytes.
A;Reference number: I48655; MUID:93346725; PMID:8345183
A;Accession: I48655
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 2162-2204,'D',2206-2213,'EY',2216-2279 <RE2>
A;Cross-references: EMBL:X69869; NID:g53055; PIDN:CAA49502.1; PID:g53056
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
C;Keywords: basement membrane; calcium binding; coiled coil; extracellular matrix; glyc
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-3106/Product: laminin alpha-2 chain #status predicted <MAT>
F;283-337/Domain: laminin-type EGF-like homology <LE01>
F;340-407/Domain: laminin-type EGF-like homology <LE02>
F;410-462/Domain: laminin-type EGF-like homology <LE03>
F;465-511/Domain: laminin-type EGF-like homology <LE04>
F;514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;720-750/Domain: laminin-type EGF-like homology <LE06>
F;753-800/Domain: laminin-type EGF-like homology <LE07>
F;803-858/Domain: laminin-type EGF-like homology <LE08>
F;861-911/Domain: laminin-type EGF-like homology <LE09>
F;914-960/Domain: laminin-type EGF-like homology <LE10>
F;963-1007/Domain: laminin-type EGF-like homology <LE11>
F;1010-1053/Domain: laminin-type EGF-like homology <LE12>
F;1056-1099/Domain: laminin-type EGF-like homology <LE13>
F;1102-1121/Domain: laminin-type EGF-like homology #status atypical <LE14>
F;1123-1159/Domain: laminin-type EGF-like homology #status atypical <LE15>
F;1162-1171/Domain: laminin-type EGF-like homology #status atypical <LE16>
F;1376-1413/Domain: laminin-type EGF-like homology #status atypical <LE17>
F;1416-1462/Domain: laminin-type EGF-like homology <LE18>
F;1465-1520/Domain: laminin-type EGF-like homology <LE19>
F;1523-1567/Domain: laminin-type EGF-like homology <LE20>
F;2166-2327/Domain: laminin G repeat homology <LG1>
F;2360-2520/Domain: laminin G repeat homology <LG2>
F;2546-2709/Domain: laminin G repeat homology <LG3>
F;2785-2933/Domain: laminin G repeat homology <LG4>
F;2960-3106/Domain: laminin G repeat homology <LG5>

  Query Match             12.9%;  Score 144.5;  DB 1;  Length 3106;
  Best Local Similarity   25.4%;  Pred. No. 0.00028;
  Matches   61;  Conservative   34;  Mismatches   86;  Indels   59;  Gaps   11;

Qy          3 NLKKTSG------------VVRLNDTVGVTKKCSEDWKLVRTASFSRGG--QMSFTNLD 47
              |:|| ||              ::   | ||||| ||   : | | || : |  :::  ::|
Db       2484 NVKKYSGCLKDIEISRTPYNILSSPDYVGVTKGCS--LENVNTVSFPKPGFVELAAVSID 2541

Qy         48 VPSTDRFQLSFGFQTFQPSGTLL------------NHQTRTSSLLVTLEDG----HIEL 90
              | :    :::  | |   || :|              ||  :   : |  |     |:
Db       2542 VGT----EINLSFSTRNESGIILLGSGGTLTPPRRKRRQTTQAYYAIFLNKGRLEVHLSS 2597

Qy         91 STRD-SNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQ-QSL 148
              ||    | |   | : || | | |   | |:  :  |:  |  | |       : : |
Db       2598 GTRTMRKIVIKPEPNLFHDGREHSVHV-ERTRGIFTVQIDEDRRHIQNLTEEQPIEVKKL 2656

Qy        149 RLGGG------------HFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKP 195
               :||              |:||: |:::         :| |     |:| :| |:  ||
Db       2657 FVGGAPPEFQPSPLRNIPAFQGCVWNLVINSIP-----MDFAQPIAFKNADIGRCTYQKP 2711


RESULT 6
MMHUMH
laminin alpha-2 chain - human (fragment)
N;Alternate names: laminin M chain; merosin heavy chain
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: PX0082; A35899; A38970; S14461
R;Hori, H.; Kanamori, T.; Mizuta, T.; Yamaguchi, N.; Liu, Y.; Nagai, Y.
J. Biochem. 116, 1212-1219, 1994
A;Title: Human laminin M chain: Epitope analysis of its monoclonal antibodies by immuno
A;Reference number: PX0082; MUID:95221315; PMID:7535762
A;Accession: PX0082
A;Molecule type: mRNA
A;Residues: 1-1751 <HOR>
A;Cross-references: UNIPROT:P24043
A;Experimental source: placenta
R;Ehrig, K.; Leivo, I.; Argraves, W.S.; Ruoslahti, E.; Engvall, E.
Proc. Natl. Acad. Sci. U.S.A. 87, 3264-3268, 1990
A;Title: Merosin, a tissue-specific basement membrane protein, is a laminin-like protei
```

```
A;Reference number: A35899; MUID:90238994; PMID:2185464
A;Accession: A35899
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 'V',623-1751 <EHR1>
A;Cross-references: EMBL:M59832
A;Accession: A38970
A;Molecule type: protein
A;Residues: 1368-1384;1389-1406;1593-1607 <EHR2>
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in lacking 1599-V
R;Ehrig, K.; Leivo, I.; Argraves, S.W.; Ruoslahti, E.; Engvall, E.
submitted to the EMBL Data Library, December 1990
A;Description: The tissue-specific basement membrane protein merosin is a laminin-like p
A;Reference number: S14461
A;Accession: S14461
A;Molecule type: mRNA
A;Residues: 'V',623-1264,'R',1266-1751 <LEI>
A;Cross-references: EMBL:M59832; NID:g187520; PIDN:AAA63215.1; PID:g187521
C;Comment: This protein is a prominent component of the basement membrane that mediates
C;Genetics:
A;Gene: GDB:LAMA2; LAMM
A;Cross-references: GDB:132362; OMIM:156225
A;Map position: 6q22-6q23
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C;Keywords: basement membrane; calcium binding; coiled coil; extracellular matrix; glycc
F;21-58/Domain: laminin-type EGF-like homology #status atypical <LE01>
F;61-107/Domain: laminin-type EGF-like homology <LE02>
F;110-165/Domain: laminin-type EGF-like homology <LE03>
F;168-212/Domain: laminin-type EGF-like homology <LE04>
F;527-567,1071-1300/Region: 3DM and 2D9 binding
F;811-972/Domain: laminin G repeat homology <LG1>
F;1005-1165/Domain: laminin G repeat homology <LG2>
F;1191-1354/Domain: laminin G repeat homology <LG3>
F;1430-1578/Domain: laminin G repeat homology <LG4>
F;1605-1751/Domain: laminin G repeat homology <LG5>
F;120,238,255,341,451,542,557,561,658,669,686,767,881,1001,1076,1119,1192,1199,1289,1509

  Query Match             12.0%;  Score 134.5;  DB 1;  Length 1751;
  Best Local Similarity   27.2%;  Pred. No. 0.0011;
  Matches   65;  Conservative   31;  Mismatches   84;  Indels   59;  Gaps   11;

Qy           3 NLKKTSG-------------VVRLNDTVGVTKKCSEDWKLVRTASFSRGG--QMSFTNLD 47
               |||| ||              ::   | ||||| ||   : | | || : |  ::|   :|
Db        1129 NLKKYSGCLKDIEISRTPYNILSSPDYVGVTKGCS--LENVYTVSFPKPGFVELSPVPID 1186

Qy          48 VPSTDRFQLSFGFQTFQPSGTLL-------------NHQTRTSSLLVTLEDGHIE--LST 92
               | :    :::  | |   || :|              ||  :  :: |  | :|  |||
Db        1187 VGT----EINLSFSTKNESGIILLGSGGTPAPPRRKRRQTGQAYYVILLNRGRLEVHLST 1242

Qy          93 ---RDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQ-QSL 148
                  | |   |  : ||  | | |   | |:  :  |:  |  | |       : : |
Db        1243 GARTMRKIVIRPEPNLFHDGREHSVHV-ERTRGIFTVQVDENRRYMQNLTVEQPIEVKKL 1301

Qy         149 RLGGG-------------HFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNK 194
                :||               ||||| |:::         :| |   : |:| :| |:  |
Db        1302 FVGGAPPEFQPSPLRNIPPPEGCIWNLVINSVP-----MDFARPVSFKNADIGRCAHQK 1355


RESULT 7
T43291
laminin alpha chain - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43291
R;Zhu, X.; Kao, G.; Joh, K.; Hall, D.H.; Wadsworth, V.K.; Hutter, H.; Vogel, B.E.; Huang
submitted to the EMBL Data Library, June 1998
A;Description: Expression, function and evolution of laminin alpha chains.
A;Reference number: Z22397
A;Accession: T43291
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3102 <ZHU>
A;Cross-references: UNIPROT:O45614; EMBL:AF074902; PIDN:AAC26793.1
C;Genetics:
A;Map position: 1
A;Note: lama1/2
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

  Query Match             10.3%;  Score 115.5;  DB 2;  Length 3102;
  Best Local Similarity   23.1%;  Pred. No. 0.13;
  Matches   53;  Conservative   39;  Mismatches   70;  Indels   67;  Gaps   11;

Qy           6 KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQP 65
               || |  :::   ||| |            | : | :    : : ::  |  :| |:| :
Db        2640 KTDGCSQVS---GVTDK---------IIGFPKPGYLITKGISIDNSSTF--AFSFRTREE 2685

Qy          66 SGTLLNHQTRTSSLLVTLED------GHI--------------ELSTRDSNIPIFKSPG 104
               :|||:   ::     |:  |      |:|              : |:|   :  |:|
Db        2686 NGTLVYQSSKLQK--VSKRDSEDDGKGYIAFYLFRGYLVLHFGKDASSR-KEVVTFRSSH 2742

Qy         105 TYMDGLLHHVSVISDTSGLRLLIDDQVLRRNQRL---PSFSNAQQSLRLGG--------- 152
                | || :| | :  :   : : :||: :  :| |     |      | |||
Db        2743 PYNDGQVHAVFMERNGKIISVKVDDKEIGDSQSLSDETSVGTTSGRLILGGFSDDLKPPN 2802

Qy         153 ------GHFEGCISNVL--VQRFSQSPEVLDLASKSTKKDASLGGCSLN 193
                     | ||||:|   ::| | :||         | :| :| ||::
Db        2803 NEIPITSFFIGCISDVFLNMKRVSLAPE---------KHNAQIGMCSMD 2842


RESULT 8
MMMSA
laminin alpha-1 chain precursor - mouse
N;Alternate names: laminin chain A1
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: A31771; A30449; S00624; A30450; S08895; S02678; S01790; A30451; S14670
R;Sasaki, M.; Kleinman, H.K.; Huber, H.; Deutzmann, R.; Yamada, Y.
J. Biol. Chem. 263, 16536-16544, 1988
A;Title: Laminin, a multidomain protein. The A chain has a unique globular domain and hc
A;Reference number: A31771; MUID:89034134; PMID:3182802
A;Accession: A31771
A;Molecule type: mRNA
A;Residues: 1-3084 <SAS>
A;Cross-references: UNIPROT:P19137; EMBL:J04064; NID:g309419; PIDN:AAA39410.1; PID:g3094
A;Accession: A30449
A;Molecule type: protein
A;Residues: 183-195;570-571,'A',573-586;596-612,'X',614-617,'EMK';630-646;1217-1222,'YPF
2486;2624-2639;2818-2843;3009-3033,'V',3035 <SA2>
R;Hartl, L.; Oberbaeumer, I.; Deutzmann, R.
Eur. J. Biochem. 173, 629-635, 1988
A;Title: The N terminus of laminin A chain is homologous to the B chains.
A;Reference number: S00624; MUID:88225080; PMID:3267223
A;Accession: S00624
A;Molecule type: mRNA
A;Residues: 1-208,'T',210-334 <HAR>
A;Cross-references: EMBL:X07737; NID:g52857; PIDN:CAA30561.1; PID:g52858
A;Accession: A30450
A;Molecule type: protein
A;Residues: 311-335,'N',337-339;630-642,'D',644;692-734;737-748,'X',750-760,'G',762-763,
3-1389;1449-1459 <HA2>
A;Note: the sequence from Fig. 7 is inconsistent with that from Fig. 5 in having 209-Ile
R;Mann, K.; Deutzmann, R.; Timpl, R.
Eur. J. Biochem. 178, 71-80, 1988
A;Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th
A;Reference number: S08895; MUID:89078415; PMID:2462498
A;Accession: S08895
A;Molecule type: protein
A;Residues: 153-169 <MAN>
R;Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.
Biochem. J. 252, 453-461, 1988
A;Title: Structure and distribution of N-linked oligosaccharide chains on various domain
A;Reference number: S02678; MUID:88326259; PMID:2458101
A;Accession: S02678
```

```
A;Molecule type: protein
A;Residues: 630-642,'D',644;2690-2704 <FUJ>
R;Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaeumer, I.; Hartl, L.
Eur. J. Biochem. 177, 35-45, 1988
A;Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te
A;Reference number: S01790; MUID:89030693; PMID:3181157
A;Accession: S01790
A;Molecule type: mRNA
A;Residues: 2538-3084 <DEU>
A;Cross-references: EMBL:X13459; NID:g55499; PIDN:CAA31807.1; PID:g818014
A;Accession: A30451
A;Molecule type: protein
A;Residues: 1911-1929;1997-2006;2033-2045,'X',2047-2054,'X',2056-2066,'X',2068-2105;2120
470;2487-2498;2502-2525;2538-2557;2561-2591,'X',2593-2594;2600-2610;2616-2645;2648-2655;
93;2998-3005,'A',3007-3033,'V',3035;3068-3083 <DE2>
A;Note: 2256-Val was also found
R;Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
Lab. Invest. 60, 772-782, 1989
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A;Reference number: A34961; MUID:89280632; PMID:2733383
A;Accession: S14670
A;Molecule type: protein
A;Residues: 2424-2436;2440-2451;2461-2467;2487-2525;2550-2557;2561-2593;2600-2610;2616-2
-2942,'T',2944-2964;2969-2976;2980-2993;2998-3000,'I',3002-3018,'V',3020-3034;3068-3083
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-3084/Product: laminin alpha-1 chain #status predicted <MAT>
F;25-277/Domain: VI <DOM6>
F;277-331/Domain: laminin-type EGF-like homology <LE01>
F;278-519/Domain: V <DOM5>
F;334-401/Domain: laminin-type EGF-like homology <LE02>
F;404-458/Domain: laminin-type EGF-like homology <LE03>
F;461-507/Domain: laminin-type EGF-like homology <LE04>
F;510-519/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;520-715/Domain: IVb <DO4B>
F;716-1166/Domain: IIIb <DO3B>
F;716-746/Domain: laminin-type EGF-like homology #status atypical <LE06>
F;749-795/Domain: laminin-type EGF-like homology <LE07>
F;798-853/Domain: laminin-type EGF-like homology <LE08>
F;830-834/Region: cell adhesion #status predicted
F;856-906/Domain: laminin-type EGF-like homology <LE09>
F;909-955/Domain: laminin-type EGF-like homology <LE10>
F;958-1002/Domain: laminin-type EGF-like homology <LE11>
F;1005-1048/Domain: laminin-type EGF-like homology <LE12>
F;1051-1094/Domain: laminin-type EGF-like homology <LE13>
F;1097-1116/Domain: laminin-type EGF-like homology #status atypical <LE14>
F;1118-1154/Domain: laminin-type EGF-like homology #status atypical <LE15>
F;1147-1149/Region: cell attachment (R-G-D) motif
F;1157-1166/Domain: laminin-type EGF-like homology #status atypical <LE16>
F;1167-1368/Domain: IVa <DO4A>
F;1369-1561/Domain: IIIa <DO3A>
F;1369-1407/Domain: laminin-type EGF-like homology #status atypical <LE17>
F;1410-1456/Domain: laminin-type EGF-like homology <LE18>
F;1459-1513/Domain: laminin-type EGF-like homology <LE19>
F;1516-1560/Domain: laminin-type EGF-like homology <LE20>
F;1562-2133/Domain: II/I <DOM2>
F;1562-2133/Region: heptad repeats
F;2134-3084/Domain: G <DOMG>
F;2150-2308/Domain: laminin G repeat homology <LG1>
F;2337-2492/Domain: laminin G repeat homology <LG2>
F;2518-2683/Domain: laminin G repeat homology <LG3>
F;2748-2897/Domain: laminin G repeat homology <LG4>
F;2925-3082/Domain: laminin G repeat homology <LG5>
F;25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;45,79,370,374,531,562,672,808,914,959,969,1052,1344,1414,1586,1603,1659,1686,1706,1718
e (Asn) (covalent) #status predicted
F;304-312/Disulfide bonds: #status experimental
F;770,857,1999,2055,2067,2835/Binding site: carbohydrate (Asn) (covalent) #status experi
F;845,2102/Binding site: carbohydrate (Asn) (covalent) #status absent
```

```
  Query Match             10.0%;  Score 111.5;  DB 1;  Length 3084;
  Best Local Similarity   20.2%;  Pred. No. 0.31;
  Matches   53;  Conservative   39;  Mismatches   75;  Indels   95;  Gaps   11;

Qy          1 MKNLK-KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFG 59
              :|||:    |    | :: || | |:   : ::: || |||      :::|
Db       2466 IKNLEISRSTFDLLRNSYGVRKGCA--LEPIQSVSFLRGGY-----VEMPP--------- 2509

Qy         60 FQTFQPSGTLL-NHQTRTSS--LLVTLEDGHIELSTRDSNIPIFK-------------- 101
               ::  |  :||     |: ||  ||| |      |      :::| |
Db       2510 -KSLSPESSLLATFATKNSSGILLVALGKDAEEAGGAQAHVPPFSIMLLEGRIEVHVNSG 2568

Qy        102 -----------SPGTYMDGLLHHVSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQQSLR 149
                        |:| ||  | :|:: :   : : :|:              |:   ::
Db       2569 DGTSLRKALLHAPTGSYSDGQEHSISLVRNRRVITIQVDE------------NSPVEMK 2615

Qy        150 LG--------------GG-------------HFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||             ||             | ||| ||::       ::||    :
Db       2616 LGPLTEGKTIDISNLYIGGLPEDKATPMLKMRTSFHGCIKNVVL-----DAQLLDFTHAT 2670

Qy        181 TKKDASLGGCSLNKPPFLMLFK 202
                :   |  | | : |   | :
Db       2671 GSEQVELDTCLLAEEPMQSLHR 2692
```

```
RESULT 9
T00021
DN-cadherin - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C;Accession: T00021
R;Iwai, Y.; Usui, T.; Hirano, S.; Steward, R.; Takeichi, M.; Uemura, T.
Neuron 19, 77-89, 1997
A;Title: Axon patterning requires DN-cadherin, a novel neuronal adhesion receptor, in t
A;Reference number: Z14058; MUID:97388431; PMID:9247265
A;Accession: T00021
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3097 <IWA>
A;Cross-references: UNIPROT:O15943; EMBL:AB002397; NID:g2381491; PIDN:BAA22151.1; PID:g
A;Experimental source: whole embryo and adult head
C;Genetics:
A;Cross-references: FlyBase:FBgn0015609
A;Map position: 36D
A;Note: l(2)36Da
F;2346-2377/Domain: EGF homology <EGF>
F;2869-2902/Domain: EGF homology <EGF1>

  Query Match              9.6%;  Score 107;  DB 2;  Length 3097;
  Best Local Similarity   21.1%;  Pred. No. 0.81;
  Matches   50;  Conservative   34;  Mismatches   69;  Indels   84;  Gaps   11;

Qy         17 VGVT-KKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLL----- 70
               || |  :| :      | ||   |   :  |::   |   ||  | | :| | ::
Db       2370 VGYTGPRCQQ-----TTRSFRGNGWAWYPPLEM--CDESHLSLEFITRKPDGLIIYNGPI 2422

Qy         71 ----NHQTRTSS-----------LLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHV 114
                   :|  |                ||:    | :||           |:  |  ||  | :
Db       2423 VPPERDETLISDFIALELERGYPRLLIDFGSGTLELRV--------KTKKTLDDGEWHRI 2474

Qy        115 SVISDTSGLRLLI------------------DDQVLRRNQRLPSFS---NAQQSLRLGG 152
               :  ||  :|:::                 ||   :   ::| |:   |    |::||
Db       2475 DLFWDTESIRMVVDFCKSAEIAEMEDGTPPEFDDMSCQARGQIPPFNEYLNVNAPLQVGG 2534

Qy        153 GH------------------FEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGC 190
               :                  |:||| |::      : :: |||     :: |: ||
Db       2535 LYREQFDQSLYFWHYMPTAKGFDGCIRNLV-----HNSKLYDLAHPGLSRN-SVAGC 2585


RESULT 10
IJFFTM
cadherin-related tumor suppressor precursor - fruit fly (Drosophila melanogaster)
```

```
C;Species: Drosophila melanogaster
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
C;Accession: A41087; B41087
R;Mahoney, P.A.; Weber, U.; Onofrechuk, P.; Biessmann, H.; Bryant, P.J.; Goodman, C.S.
Cell 67, 853-868, 1991
A;Title: The fat tumor suppressor gene in Drosophila encodes a novel member of the cadhe
A;Reference number: A41087; MUID:92069752; PMID:1959133
A;Accession: A41087
A;Molecule type: mRNA
A;Residues: 143-485;1279-5147 <MAH>
A;Cross-references: GB:M80537
A;Accession: B41087
A;Molecule type: DNA
A;Residues: 1-142;487-1278 <MA2>
A;Cross-references: GB:M80537
A;Note: 1229-Gly and 1233-Ser were also found
C;Genetics:
A;Gene: fat
A;Cross-references: FlyBase:FBgn0001075
C;Superfamily: cadherin-related tumor suppressor; cadherin repeat homology; EGF homology
C;Keywords: calcium binding; cell adhesion; duplication; transmembrane protein
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-5147/Product: cadherin-related tumor suppressor #status predicted <MAT>
F;36-4583/Domain: extracellular #status predicted <EXT>
F;51-156/Domain: cadherin repeat homology <CR1>
F;159-270/Domain: cadherin repeat homology <CR2>
F;271-382/Domain: cadherin repeat homology <CR3>
F;390-494/Domain: cadherin repeat homology <CR4>
F;497-599/Domain: cadherin repeat homology <CR5>
F;602-708/Domain: cadherin repeat homology <CR6>
F;718-822/Domain: cadherin repeat homology <CR7>
F;831-942/Domain: cadherin repeat homology <CR8>
F;948-1049/Domain: cadherin repeat homology <CR9>
F;1052-1153/Domain: cadherin repeat homology <C10>
F;1156-1278/Domain: cadherin repeat homology <C11>
F;1281-1384/Domain: cadherin repeat homology <C12>
F;1387-1489/Domain: cadherin repeat homology <C13>
F;1492-1601/Domain: cadherin repeat homology <C14>
F;1607-1713/Domain: cadherin repeat homology <C15>
F;1717-1823/Domain: cadherin repeat homology <C16>
F;1826-1922/Domain: cadherin repeat homology <C17>
F;1925-2027/Domain: cadherin repeat homology <C18>
F;2028-2167/Domain: cadherin repeat homology <C19>
F;2169-2278/Domain: cadherin repeat homology <C20>
F;2281-2384/Domain: cadherin repeat homology <C99>
F;2387-2491/Domain: cadherin repeat homology <C21>
F;2494-2596/Domain: cadherin repeat homology <C22>
F;2599-2703/Domain: cadherin repeat homology <C23>
F;2707-2810/Domain: cadherin repeat homology <C24>
F;2813-2913/Domain: cadherin repeat homology <C25>
F;2915-3013/Domain: cadherin repeat homology <C26>
F;3014-3124/Domain: cadherin repeat homology <C27>
F;3127-3229/Domain: cadherin repeat homology <C28>
F;3232-3334/Domain: cadherin repeat homology <C29>
F;3337-3439/Domain: cadherin repeat homology <C30>
F;3442-3545/Domain: cadherin repeat homology <C31>
F;3548-3651/Domain: cadherin repeat homology <C32>
F;3654-3756/Domain: cadherin repeat homology <C33>
F;3954-4010/Domain: EGF homology <EG1>
F;4017-4048/Domain: EGF homology <EG2>
F;4056-4089/Domain: EGF homology <EG3>
F;4096-4127/Domain: EGF homology <EG4>
F;4584-4609/Domain: transmembrane #status predicted <TMM>
F;4610-5147/Domain: intracellular #status predicted <INT>

  Query Match              9.4%;  Score 105;  DB 1;  Length 5147;
  Best Local Similarity   24.4%;  Pred. No. 2.5;
  Matches   38;  Conservative   30;  Mismatches   64;  Indels   24;  Gaps    6;

Qy         33 ASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELST 92
              ::||   |:     : |      ||  |:|::  | :|   |      ::| :| :   :
Db       4413 SNFSTASQI----YEAPK----MLSMLFRTYKDQGQILYAATNQMFTSLSLREGRLVYYS 4464

Qy         93 RDS---NIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQQS-- 147
              :     |: : :   |  ||  |:||: |::  |||::| : :     :    :
Db       4465 KQHLTINMTV-QETSTLNDGKWHNVSLFSESRSLRLIVDGRQVGDELDIAGVHDFLDPYL 4523

Qy        148 --LRLGGGHFEGCISNVLVQRFSQS--------PEV 173
               | :||  | ||::|| |     |          |||
Db       4524 TILNVGGEAFVGCLANVTVNNELQPLNGSGSIFPEV 4559


RESULT 11
S14458
laminin alpha-1 chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S14458; S14663; A34961
R;Haaparanta, T.; Uitto, J.; Ruoslahti, E.; Engvall, E.
Matrix 11, 151-160, 1991
A;Title: Molecular cloning of the cDNA encoding human laminin A chain.
A;Reference number: S14458; MUID:91333420; PMID:1714537
A;Accession: S14458
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-3075 <HAA>
A;Cross-references: UNIPROT:P25391
R;Nissinen, M.; Vuolteenaho, R.; Boot-Handford, R.; Kallunki, P.; Tryggvason, K.
Biochem. J. 276, 369-379, 1991
A;Title: Primary structure of the human laminin A chain. Limited expression in human tis
A;Reference number: S14663; MUID:91264789; PMID:2049067
A;Accession: S14663
A;Molecule type: mRNA
A;Residues: 1-227,'FE',230-251,'MLP',255-418,'E',420-518,'L',520-1022,'V',1024-1074,'V',
A;Cross-references: EMBL:X58531; NID:g34225; PIDN:CAA41418.1; PID:g34226
R;Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
Lab. Invest. 60, 772-782, 1989
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A;Reference number: A34961; MUID:89280632; PMID:2733383
A;Accession: A34961
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 'W',2397-2745,'L',2747-3053,'L',3055-3072,'PSP' <OLS>
A;Note: the authors translated the codon AGA for residue 2692 as Pro
C;Genetics:
A;Gene: GDB:LAMA1; LAMA
A;Cross-references: GDB:120135; OMIM:150320
A;Map position: 18p11.32-18p11.22
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; disulfide bon
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-3075/Product: laminin alpha-1 chain #status predicted <MAT>
F;18-269/Domain: VI <DOM6>
F;270-516/Domain: V <DOM5>
F;270-324/Domain: laminin-type EGF-like homology <LE1>
F;327-394/Domain: laminin-type EGF-like homology <LE2>
F;397-451/Domain: laminin-type EGF-like homology <LE3>
F;454-500/Domain: laminin-type EGF-like homology <LE4>
F;503-512/Domain: laminin-type EGF-like homology #status atypical <LE5>
F;517-708/Domain: IVb <DO4B>
F;709-1159/Domain: IIIb <DO3B>
F;709-739/Domain: laminin-type EGF-like homology #status atypical <LE6>
F;742-788/Domain: laminin-type EGF-like homology <LE7>
F;791-846/Domain: laminin-type EGF-like homology <LE8>
F;849-899/Domain: laminin-type EGF-like homology <LE9>
F;902-948/Domain: laminin-type EGF-like homology <LE10>
F;951-995/Domain: laminin-type EGF-like homology <LE11>
F;998-1041/Domain: laminin-type EGF-like homology <LE12>
F;1044-1087/Domain: laminin-type EGF-like homology <LE13>
F;1090-1109/Domain: laminin-type EGF-like homology #status atypical <LE14>
F;1111-1147/Domain: laminin-type EGF-like homology #status atypical <LE15>
F;1150-1159/Domain: laminin-type EGF-like homology #status atypical <LE16>
F;1160-1361/Domain: IVa <DO4A>
F;1362-1553/Domain: IIIa <DO3A>
F;1362-1400/Domain: laminin-type EGF-like homology #status atypical <LE17>
F;1403-1449/Domain: laminin-type EGF-like homology <LE18>
```

```
F;1452-1506/Domain: laminin-type EGF-like homology <LE19>
F;1509-1553/Domain: laminin-type EGF-like homology <LE20>
F;1554-2125/Domain: I/II, heptad repeats <DOM2>
F;2116-2120/Region: cell adhesion #status predicted
F;2126-3075/Domain: G <DOMG>
F;2142-2300/Domain: laminin G repeat homology <LG1>
F;2329-2484/Domain: laminin G repeat homology <LG2>
F;2510-2676/Domain: laminin G repeat homology <LG3>
F;2534-2536/Region: cell attachment (R-G-D) motif
F;2739-2888/Domain: laminin G repeat homology <LG4>
F;2916-3073/Domain: laminin G repeat homology <LG5>
F;38,164,555,665,763,801,838,926,952,1045,1407,1579,1596,1678,1689,1698,1717,1804,1894,1
rate (Asn) (covalent) #status predicted
F;297-305/Disulfide bonds: #status predicted

  Query Match             9.1%;  Score 101.5;  DB 2;  Length 3075;
  Best Local Similarity   21.3%;  Pred. No. 2.6;
  Matches   53;  Conservative   43;  Mismatches  102;  Indels   51;  Gaps   10;

Qy          1 MKNLK-KTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFG 59
              :|||:    |    | :: || | |   : :|: || :|| :     :     : ::|
Db       2458 IKNLEISRSTFDLLRNSYGVRKGCL--LEPIRSVSFLKGGYIELPPKSLSPESEWLVTFA 2515

Qy         60 FQTFQPSGTLL-----------NHQTRTSSLLVTLEDGHIELSTRDSN-----IPIFKS 102
                |   || :|              :       | |  |:||:     :       :  :
Db       2516 --TTNSSGIILAALGGDVEKRGDREEAHVPFFSVMLIGGNIEVHVNPGDGTGLRKALLHA 2573

Qy        103 P-GTYMDGLLHHVSVISDTSGLRLLIDDQ---VLRRNQRLPSFSNAQQSLRLGG------ 152
              | ||  ||  | :|:: :   : : :|:     ::    : | :    :| :||
Db       2574 PTGTCSDGQAHSISLVRNRRIITVQLDENNPVEMKLGTLVESRTINVSNLYVGGIPEGEG 2633

Qy        153 -------GHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFL------- 198
                    | ||| |::      : |:||  |    :   |  | |:: | |
Db       2634 TSLLTMRRSFHGCIKNLIF-----NLELLDFNSAVGHEQVDLDTCWLSERPKLAPDAEDS 2688

Qy        199 MLFKSPKRF 207
               | : |: |
Db       2689 KLLREPRAF 2697


RESULT 12
T23433
hypothetical protein K08C7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23433
R;Berks, M.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19740
A;Accession: T23433
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3672 <WIL>
A;Cross-references: UNIPROT:Q21313; EMBL:Z70286; PIDN:CAA94293.1; GSPDB:GN00022; CESP:KC
A;Experimental source: clone K08C7
C;Genetics:
A;Gene: CESP:K08C7.3
A;Map position: 4
A;Introns: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 3
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

  Query Match             8.9%;  Score 99.5;  DB 2;  Length 3672;
  Best Local Similarity   27.1%;  Pred. No. 5;
  Matches   60;  Conservative   31;  Mismatches   79;  Indels   51;  Gaps   12;

Qy          1 MKNLKKTSGVVRLND---TVGVTKKCSEDWKLVRTASF-SRGGQMSFTNLDVPSTDRFQL 56
              :|::|  |  | |      : ||    |       ||| || |      || |    | |   :
Db       3041 IKSVKLGSDNVDLESSHASKGVRSGC--PLHSVRTVSFLSDRTTASFNNATEFSED-VSV 3097

Qy         57 SFGFQT---FQPSGTLLNHQTRTSSLLVTL-EDGHIELSTRD--SNIPIFKSPGTYMDGL 110
              :| |:|     |||      :    | | |:: ||| : ::: :  : : :  ||    |
Db       3098 TFKFKTRSIRQPSSLFTVNDDEDSVLSVSINEDGILTVTSGEDIATLELAASP----DEK 3153

Qy        111 LHHVSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGH---------------- 154
              |:||:      :|:  ||          ||||          :
Db       3154 WHYVSIRKTKYIIRIDADD----------SFSNEVARKHADDSNPDASFLSAFFGKSGET 3203

Qy        155 --FEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 193
               | ||| :| :     : ::|| |: |  |: || ||||:
Db       3204 PSFVGCIGDVTL-----NGKLLDFAN-SEIKEISLNGCSLS 3238


RESULT 13
T37316
probable laminin alpha chain - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37316
R;Joh, K.; Zhu, K.; Hedgecock, E.M.; Inoue, T.; Hori, K.
submitted to the EMBL Data Library, August 1998
A;Description: Laminin alpha chain gene in the nematode C. elegans.
A;Reference number: Z21681
A;Accession: T37316
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3704 <JOH>
A;Cross-references: UNIPROT:P91904; EMBL:AB016806; PIDN:BAA32347.1
A;Experimental source: strain N2
C;Genetics:
A;Gene: epi-1
A;Map position: IV
A;Introns: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3;
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like

  Query Match             8.9%;  Score 99.5;  DB 2;  Length 3704;
  Best Local Similarity   27.1%;  Pred. No. 5.1;
  Matches   60;  Conservative   31;  Mismatches   79;  Indels   51;  Gaps   12;

Qy          1 MKNLKKTSGVVRLND---TVGVTKKCSEDWKLVRTASF-SRGGQMSFTNLDVPSTDRFQL 56
              :|::|  |  | |      : ||    |       ||| || |      || |    | |   :
Db       3041 IKSVKLGSDNVDLESSHASKGVRSGC--PLHSVRTVSFLSDRTTASFNNATEFSED-VSV 3097

Qy         57 SFGFQT---FQPSGTLLNHQTRTSSLLVTL-EDGHIELSTRD--SNIPIFKSPGTYMDGL 110
              :| |:|     |||      :    | | |:: ||| : ::: :  : : :  ||    |
Db       3098 TFKFKTRSIRQPSSLFTVNDDEDSVLSVSINEDGILTVTSGEDIATLELAASP----DEK 3153

Qy        111 LHHVSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGH---------------- 154
              |:||:      :|:  ||          ||||          :
Db       3154 WHYVSIRKTKYIIRIDADD----------SFSNEVARKHADDSNPDASFLSAFFGKSGET 3203

Qy        155 --FEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLN 193
               | ||| :| :     : ::|| |: |  |: || ||||:
Db       3204 PSFVGCIGDVTL-----NGKLLDFAN-SEIKEISLNGCSLS 3238


RESULT 14
E86327
protein F18O14.19 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86327
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E86327
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1158 <STO>
```

```
A;Cross-references: UNIPROT:Q9LN51; GB:AE005172; NID:g8778419; PIDN:AAF79427.1; GSPDB:GN
C;Genetics:
A;Gene: F18O14.19
A;Map position: 1

  Query Match             8.9%;  Score 99;  DB 2;  Length 1158;
  Best Local Similarity   26.1%;  Pred. No. 1.2;
  Matches   35;  Conservative   22;  Mismatches   51;  Indels   26;  Gaps    4;

Qy         15 DTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQT 74
              | ||::    :||||::     |  :          ||:|    | |:::    :  || |
Db        135 DLVGISGLNDDDWKLLQHMLAERKNK---------STERLSGKFFFESWIIDTSASNHMT 185

Qy         75 RT----------SSLLVTLEDGHIELSTRDSNIPIFKSPGT----YMDGLLHH---VSVI 117
               |          : :|: | ||    ||:   : :  |        ::|||  |   || :
Db        186 GTLEFLLDIHGMAPVLIKLPDGRFTTSTKHGRVLMGSSLSLQDVFFVDGLHCHLISVSQL 245

Qy        118 SDTSGLRLLIDDQV 131
              :  ||    | |:|
Db        246 TRDSGYMFQITDKV 259


RESULT 15
KXBOS
plasma protein S precursor - bovine
N;Alternate names: vitamin K-dependent protein S
C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Aug-1987 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004
C;Accession: A24759; A23888
R;Dahlback, B.; Lundwall, A.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 83, 4199-4203, 1986
A;Title: Primary structure of bovine vitamin K-dependent protein S.
A;Reference number: A24759; MUID:86233400; PMID:2940598
A;Accession: A24759
A;Molecule type: mRNA
A;Residues: 1-675 <DAH>
A;Cross-references: UNIPROT:P07224; GB:M13044; NID:g163697; PIDN:AAA30757.1; PID:g163698
A;Note: parts of this sequence, including the amino end of the mature protein, were dete
R;Dahlback, B.; Lundwall, A.; Stenflo, J.
J. Biol. Chem. 261, 5111-5115, 1986
A;Title: Localization of thrombin cleavage sites in the amino-terminal region of bovine
A;Reference number: A23888; MUID:86168236; PMID:2937785
A;Accession: A23888
A;Molecule type: protein
A;Residues: 42-141 <DA2>
C;Complex: in plasma forms a complex with C4b binding protein
C;Function:
A;Description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage dest
C;Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
C;Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coagulation; carbox
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-41/Domain: propeptide #status predicted <PRO>
F;26-85/Domain: Gla domain homology <GLA>
F;42-675/Product: plasma protein S #status experimental <MAT>
F;121-154/Domain: EGF homology <EG1>
F;161-199/Domain: EGF homology <EG2>
F;205-241/Domain: EGF homology <EG3>
F;247-282/Domain: EGF homology <EG4>
F;315-666/Domain: sex hormone-binding globulin homology <SHB>
F;325-478/Domain: laminin G repeat homology <LGR>
F;47,48,55,57,60,61,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F;58-63,88-113,121-134,126-143,145-154,161-175,171-184,186-199,205-217,212-226,228-241,2
F;93-94/Cleavage site: Arg-Ala (thrombin) #status experimental
F;111-112/Cleavage site: Arg-Ser (thrombin) #status experimental
F;136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;177,219,258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
F;288-567,449-475,638-665/Disulfide bonds: #status experimental
F;499/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;509/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             8.5%;  Score 94.5;  DB 1;  Length 675;
  Best Local Similarity   29.6%;  Pred. No. 1.4;
  Matches   24;  Conservative   15;  Mismatches   39;  Indels    3;  Gaps    2;

Qy         39 GQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSS--LLVTLEDGHIELSTRDSN 96
              | : :    :| | ||   | |:|:   | :|  ::   |   |: | :| ||:  ::
Db        308 GVVLYLKFRLPETTRFSAEFDFRTYDSEGVILYAESSDHSAWFLIALREGKIEIQFKNEK 367

Qy         97 IPIFKSPGTYM-DGLLHHVSV 116
                 : |  : ||| | |||
Db        368 TTKMTTGGKVINDGLWHMVSV 388


Search completed: February 22, 2005, 08:19:40
Job time : 7.81686 secs
```

GenCore version 5.1.6

QM protein - protein search, using sw model

Run on: February 22, 2005, 08:07:29 ; Search time 36.8842 Seconds
(without alignments)
3026.590 Million cell updates/sec

Title: US-10-817-423-6
Perfect score: 1118
Sequence: 1 MKNLKKTSGVVRLNDTVGVT.....MLFKSPKRFNKGRIFNVNQL 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1118	100.0	1725	2	P70570	P70570 rattus norv
2	1033	92.4	3333	1	LMA3_MOUSE	Q61789 mus musculu
3	852	76.2	1668	2	Q6VU69	Q6vu69 homo sapien
4	852	76.2	3277	2	Q6VU67	Q6vu67 homo sapien
5	852	76.2	3333	2	Q6VU68	Q6vu68 homo sapien
6	850	76.0	1713	1	LMA3_HUMAN	Q16787 homo sapien
7	850	76.0	1806	2	Q96TG0	Q96tg0 homo sapien
8	850	76.0	3333	2	Q76E14	Q76e14 homo sapien
9	760.5	68.0	1725	2	Q867A1	Q867a1 canis famil
10	204	18.2	1254	2	Q91VV0	Q91vv0 mus musculu
11	204	18.2	1816	1	LMA4_MOUSE	P97927 mus musculu
12	187	16.7	1816	1	LMA4_HUMAN	Q16363 homo sapien
13	186	16.6	794	2	Q8R3Y7	Q8r3y7 mus musculu
14	186	16.6	1524	2	Q6ZQA1	Q6zqa1 mus musculu
15	186	16.6	3718	1	LMA5_MOUSE	Q61001 mus musculu
16	174	15.6	670	2	Q9BTT3	Q9btt3 homo sapien
17	174	15.6	3695	1	LMA5_HUMAN	O15230 homo sapien
18	174	15.6	3695	2	Q8TDF8	Q8tdf8 homo sapien
19	173.5	15.5	3712	1	LMA_DROME	Q00174 drosophila
20	173.5	15.5	3712	2	Q9VRW0	Q9vrw0 drosophila
21	144.5	12.9	3106	1	LMA2_MOUSE	Q60675 mus musculu
22	143.5	12.8	659	2	Q7TQI9	Q7tqi9 mus musculu
23	143.5	12.8	858	2	Q8R145	Q8r145 mus musculu
24	134.5	12.0	517	2	Q8MRJ7	Q8mrj7 drosophila
25	134.5	12.0	1039	2	Q9VQB1	Q9vqb1 drosophila
26	134.5	12.0	3110	1	LMA2_HUMAN	P24043 homo sapien
27	130.5	11.7	211	2	Q712T9	Q712t9 mus musculu
28	128.5	11.5	2923	1	CLR2_HUMAN	Q9hcu4 homo sapien
29	127	11.4	1247	2	Q7PT06	Q7pt06 anopheles g
30	124	11.1	2144	1	CLR2_RAT	Q9qyp2 rattus norv
31	122.5	11.0	2920	1	CLR2_MOUSE	Q9r0m0 mus musculu
32	122.5	11.0	3616	2	Q7PPF9	Q7ppf9 anopheles g
33	115.5	10.3	3102	2	O45614	O45614 caenorhabdi
34	111.5	10.0	3084	1	LMA1_MOUSE	P19137 mus musculu
35	110	9.8	3367	2	Q9XZC9	Q9xzc9 drosophila
36	110	9.8	3375	2	Q8IP51	Q8ip51 drosophila
37	107	9.6	3097	1	CADN_DROME	O15943 drosophila
38	105	9.4	5147	1	FAT_DROME	P33450 drosophila
39	104	9.3	1180	2	Q8BPP6	Q8bpp6 mus musculu
40	104	9.3	1310	1	CTA4_MOUSE	Q99p47 mus musculu
41	104	9.3	1310	2	Q8K002	Q8k002 mus musculu
42	104	9.3	1330	2	Q69ZB1	Q69zb1 mus musculu
43	101.5	9.1	3075	1	LMA1_HUMAN	P25391 homo sapien
44	101	9.0	1306	2	Q8WYK1	Q8wyk1 homo sapien
45	100	8.9	436	2	P91806	P91806 strongyloce

ALIGNMENTS

RESULT 1
P70570
ID P70570 PRELIMINARY; PRT; 1725 AA.
AC P70570;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Laminin-5 alpha 3 chain.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97081969; PubMed=8923212;
RA Baker S.E., Hopkinson S.B., Fitchmun M., Andreason G.L., Frasier F.,
RA Plopper G., Quaranta V., Jones J.C.R.;
RT "Laminin-5 and hemidesmosomes: role of the alpha 3 chain subunit in
RT hemidesmosome stability and assembly.";
RL J. Cell Sci. 109:2509-2520(1996).
DR EMBL; U61261; AAB17053.1; -.
DR HSSP; P35070; 1IP0.
DR GO; GO:0005606; C:laminin-1; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR GO; GO:0030334; P:regulation of cell migration; IEA.
DR GO; GO:0045995; P:regulation of embryonic development; IEA.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00053; Laminin_EGF; 2.
DR Pfam; PF02210; Laminin_G_2; 4.
DR Pfam; PF06008; Laminin_I; 1.
DR Pfam; PF06009; Laminin_II; 1.
DR SMART; SM00180; EGF_Lam; 2.
DR SMART; SM00282; LamG; 5.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW Laminin EGF-like domain.
SQ SEQUENCE 1725 AA; 190392 MW; 02EE43B33E72B0FB CRC64;

Query Match 100.0%; Score 1118; DB 2; Length 1725;
Best Local Similarity 100.0%; Pred. No. 2.1e-87;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db       1129 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 1188

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1189 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 1248

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1249 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 1308

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              |||||||||||||||||||||||||||||||||||||
Db       1309 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 1346


RESULT 2
LMA3_MOUSE
ID   LMA3_MOUSE     STANDARD;      PRT;  3333 AA.
AC   Q61789; O08751; Q61788; Q61966; Q9JHQ7;
DT   01-NOV-1997 (Rel. 35, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Laminin alpha-3 chain precursor (Nicein alpha subunit).
GN   Name=Lama3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE OF 1-58 FROM N.A., AND SEQUENCE OF 32-38.
RX   MEDLINE=21818471; PubMed=11829758; DOI=10.1042/0264-6021:3620213;
RA   Garbe J.H., Gohring W., Mann K., Timpl R., Sasaki T.;
RT   "Complete sequence, recombinant analysis and binding to laminins and
RT   sulphated ligands of the N-terminal domains of laminin alpha3B and
RT   alpha5 chains.";
RL   Biochem. J. 362:213-221(2002).
RN   [2]
RP   SEQUENCE OF 1-726 FROM N.A.
RC   STRAIN=ICR;
RX   MEDLINE=97296337; PubMed=9151674; DOI=10.1083/jcb.137.3.685;
RA   Miner J.H., Patton B.L., Lentz S.I., Gilbert D.J., Snider W.D.,
RA   Jenkins N.A., Copeland N.G., Sanes J.R.;
RT   "The laminin alpha chains: expression, developmental transitions, and
RT   chromosomal locations of alpha1-5, identification of heterotrimeric
RT   laminins 8-11, and cloning of a novel alpha3 isoform.";
RL   J. Cell Biol. 137:685-701(1997).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM A), AND SEQUENCE OF 716-3284 FROM N.A.
RP   (ISOFORM B).
RC   STRAIN=BALB/c; TISSUE=Lung;
RX   MEDLINE=95394948; PubMed=7665604; DOI=10.1074/jbc.270.37.21820;
RA   Galliano M.-F., Aberdam D., Aguzzi A., Ortonne J.-P., Meneguzzi G.;
RT   "Cloning and complete primary structure of the mouse laminin alpha 3
RT   chain. Distinct expression pattern of the laminin alpha 3A and alpha
RT   3B chain isoforms.";
RL   J. Biol. Chem. 270:21820-21826(1995).
RN   [4]
RP   REVISIONS.
RA   Aberdam D.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 1767-2485 FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=94281750; PubMed=8012114;
RA   Aberdam D., Galliano M.-F., Mattei M.-G., Pisani-Spadafora A.,
RA   Ortonne J.-P., Meneguzzi G.;
RT   "Assignment of mouse nicein genes to chromosomes 1 and 18.";
RL   Mamm. Genome 5:229-233(1994).
RN   [6]
RP   SEQUENCE OF 1767-2485 FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=94363405; PubMed=8081888;
RA   Aberdam D., Aguzzi A., Baudoin C., Galliano M.-F., Ortonne J.-P.,
RA   Meneguzzi G.;
RT   "Developmental expression of nicein adhesion protein (laminin-5)
RT   subunits suggests multiple morphogenic roles.";
RL   Cell Adhes. Commun. 2:115-129(1994).
CC   -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC       is thought to mediate the attachment, migration and organization
CC       of cells into tissues during embryonic development by interacting
CC       with other extracellular matrix components.
CC   -!- FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
CC       via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-
CC       6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine
CC       phosphorylation of pp125-FAK and p80, (3) differentiation of
CC       keratinocytes (By similarity).
CC   -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC       different polypeptide chains (alpha, beta, gamma), which are bound
CC       to each other by disulfide bonds into a cross-shaped molecule
CC       comprising one long and three short arms with globules at each
CC       end. The alpha-3 chain is a subunit of laminin-5
CC       (epiligrin/kalinin/nicein), and possibly also a component of
CC       laminin-6 (K-laminin) and laminin-7 (KS-laminin).
CC   -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC       membranes (major component).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=B;
CC         IsoId=Q61789-1; Sequence=Displayed;
CC       Name=A;
CC         IsoId=Q61789-2; Sequence=VSP_003038, VSP_003039;
CC   -!- TISSUE SPECIFICITY: Basal membrane of the upper alimentary tract
CC       and urinary and nasal epithelia, salivary glands and teeth (both
CC       variants). Isoform A is predominantly expressed in skin, hair
CC       follicles and developing neurons of the trigeminal ganglion.
CC       Isoform B was found in bronchi, alveoli, stomach, intestinal
CC       crypts, whisker pads, CNS, telencephalic neuroectoderm, thalamus,
CC       Rathke's pouch and periventricular subependymal germinal layer.
CC   -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC       with other laminin chains to form a coiled coil structure.
CC   -!- DOMAIN: Domains IV and G are globular.
CC   -!- SIMILARITY: Contains 15 laminin EGF-like domains.
CC   -!- SIMILARITY: Contains 5 laminin G-like domains.
CC   -!- SIMILARITY: Contains 1 laminin IV domain.
CC   -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ293592; CAB99254.2; -.
DR   EMBL; U88353; AAC53179.1; -.
DR   EMBL; X84014; CAA58837.1; -.
DR   EMBL; X84013; CAA58836.1; ALT_FRAME.
DR   EMBL; L20478; AAA68091.1; -.
DR   HSSP; P02468; 1NPE.
DR   MGD; MGI:99909; Lama3.
DR   GO; GO:0005604; C:basement membrane; IDA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR008212; Lam_N2.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR008211; Laminin_N.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 10.
```

```
DR   Pfam; PF00054; Laminin_G; 3.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   Pfam; PF00055; Laminin_N; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   ProDom; PD003031; Laminin_B; 1.
DR   PROSITE; PS00022; EGF_1; 10.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 10.
KW   Alternative splicing; Basement membrane; Cell adhesion; Coiled coil;
KW   Direct protein sequencing; Extracellular matrix; Glycoprotein;
KW   Laminin EGF-like domain; Repeat; Signal.
FT   SIGNAL       1     31
FT   CHAIN       32   3333       Laminin alpha-3 chain.
FT   DOMAIN      32    294       Laminin N-terminal (domain VI).
FT   DOMAIN     295    725       Domain V.
FT   DOMAIN     296    350       Laminin EGF-like 1.
FT   DOMAIN     353    420       Laminin EGF-like 2.
FT   DOMAIN     423    464       Laminin EGF-like 3.
FT   DOMAIN     488    530       Laminin EGF-like 4.
FT   DOMAIN     533    576       Laminin EGF-like 5.
FT   DOMAIN     582    625       Laminin EGF-like 6.
FT   DOMAIN     628    678       Laminin EGF-like 7.
FT   DOMAIN     681    725       Laminin EGF-like 8.
FT   DOMAIN     793   1262       Laminin domain IV 1 (domain IV B).
FT   DOMAIN    1263   1464       Domain III B.
FT   DOMAIN    1310   1353       Laminin EGF-like 9.
FT   DOMAIN    1354   1403       Laminin EGF-like 10.
FT   DOMAIN    1404   1454       Laminin EGF-like 11.
FT   DOMAIN    1455   1464       Laminin EGF-like 12 (N-terminal).
FT   DOMAIN    1465   1653       Laminin domain IV (domain IV A).
FT   DOMAIN    1654   1821       Domain III A.
FT   DOMAIN    1654   1686       Laminin EGF-like 12 (C-terminal).
FT   DOMAIN    1687   1733       Laminin EGF-like 13.
FT   DOMAIN    1734   1786       Laminin EGF-like 14.
FT   DOMAIN    1787   1821       Laminin EGF-like 15 (incomplete).
FT   DOMAIN    1822   2388       Domain II and I.
FT   DOMAIN    2389   2590       Laminin G-like 1.
FT   DOMAIN    2597   2759       Laminin G-like 2.
FT   DOMAIN    2766   2926       Laminin G-like 3.
FT   DOMAIN    2986   3150       Laminin G-like 4.
FT   DOMAIN    3157   3330       Laminin G-like 5.
FT   DOMAIN    1854   1983       Coiled coil (Potential).
FT   DOMAIN    2015   2060       Coiled coil (Potential).
FT   DOMAIN    2091   2168       Coiled coil (Potential).
FT   DOMAIN    2214   2241       Coiled coil (Potential).
FT   DOMAIN    2321   2386       Coiled coil (Potential).
FT   SITE      2277   2279       Cell attachment site (Potential).
FT   DISULFID  1310   1317       By similarity.
FT   DISULFID  1312   1324       By similarity.
FT   DISULFID  1326   1335       By similarity.
FT   DISULFID  1338   1351       By similarity.
FT   DISULFID  1354   1369       By similarity.
FT   DISULFID  1356   1376       By similarity.
FT   DISULFID  1378   1387       By similarity.
FT   DISULFID  1390   1401       By similarity.
FT   DISULFID  1404   1416       By similarity.
FT   DISULFID  1406   1423       By similarity.
FT   DISULFID  1425   1434       By similarity.
FT   DISULFID  1437   1452       By similarity.
FT   DISULFID  1687   1696       By similarity.
FT   DISULFID  1689   1703       By similarity.
FT   DISULFID  1706   1715       By similarity.
FT   DISULFID  1718   1731       By similarity.
FT   DISULFID  1734   1746       By similarity.
FT   DISULFID  1736   1755       By similarity.
FT   DISULFID  1757   1766       By similarity.
FT   DISULFID  1769   1784       By similarity.
FT   DISULFID  1822   1822       Interchain (Probable).
FT   DISULFID  1825   1825       Interchain (Probable).

  Query Match             92.4%;  Score 1033;  DB 1;  Length 3333;
  Best Local Similarity   92.7%;  Pred. No. 1.1e-79;
  Matches  202;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       2737 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSLDRFQLSFGF 2796

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              |||||||||||||||||||||||||||| |||||: ||||||||||||||||||||||||
Db       2797 QTFQPSGTLLNHQTRTSSLLVTLEDGHIALSTRDSSSPIFKSPGTYMDGLLHHVSVISDT 2856

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              |||||||||||||||||| ||||||||| :|||:|||||||| ||| |||||||:||||
Db       2857 SGLRLLIDDQVLRRNQRLASFSNAQQSLSMGGGYFEGCISNVFVQRMSQSPEVLDMASKS 2916

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              ||:|| |||||||||||||||||| ||| | ||||||
Db       2917 TKRDAFLGGCSLNKPPFLMLFKSPKGFNKARSFNVNQL 2954


RESULT 3
Q6VU69
ID   Q6VU69      PRELIMINARY;      PRT;  1668 AA.
AC   Q6VU69;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Laminin alpha 3 splice variant a.
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
RA   McLean W.H., Irvine A.D., Hamill K.J., Whittock N.V.,
RA   Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
RA   Dopping-Hepenstal P.J., Eady R.A., Jamil T., Phillips R.J.,
RA   Shabbir S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
RA   Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
RA   McGrath J.A.;
RT   "An unusual N-terminal deletion of the laminin {alpha}3a isoform leads
RT   to the chronic granulation tissue disorder laryngo-onycho-cutaneous
RT   syndrome.";
RL   Hum. Mol. Genet. 12:2395-2409(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   McLean W.H.I.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY327114; AAQ72569.1; -.
DR   GO; GO:0005606; C:laminin-1; IEA.
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00053; Laminin_EGF; 1.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   SMART; SM00180; EGF_Lam; 2.
DR   SMART; SM00282; LamG; 5.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; 1.
```

```
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Laminin EGF-like domain.
SQ   SEQUENCE   1668 AA;  184053 MW;  9EBF5FC45637645C CRC64;

  Query Match             76.2%;  Score 852;  DB 2;  Length 1668;
  Best Local Similarity   76.6%;  Pred. No. 1.9e-64;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1073 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1132

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| |||||:||||| ||  |||||| ||||||||:||||||
Db       1133 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGSPIFKSPQTYMDGLLHYVSVISDN 1192

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1193 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1252

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
               |:| |||||||||||||| |   |||| : | :|||
Db       1253 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1290


RESULT 4
Q6VU67
ID   Q6VU67      PRELIMINARY;      PRT;  3277 AA.
AC   Q6VU67;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Laminin alpha 3 splice variant b2.
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
RA   McLean W.H., Irvine A.D., Hamill K.J., Whittock N.V.,
RA   Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
RA   Dopping-Hepenstal P.J., Eady R.A., Jamil T., Phillips R.J.,
RA   Shabbir S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
RA   Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
RA   McGrath J.A.;
RT   "An unusual N-terminal deletion of the laminin {alpha}3a isoform leads
RT   to the chronic granulation tissue disorder laryngo-onycho-cutaneous
RT   syndrome.";
RL   Hum. Mol. Genet. 12:2395-2409(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   McLean W.H.I.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY327116; AAQ72571.1; -.
DR   GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR   GO; GO:0005606; C:laminin-1; IEA.
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR008211; Laminin_N.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 8.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   Pfam; PF00055; Laminin_N; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   ProDom; PD003031; Laminin_B; 1.
DR   SMART; SM00181; EGF; 8.
DR   SMART; SM00180; EGF_Lam; 14.
DR   SMART; SM00281; LamB; 1.
DR   SMART; SM00282; LamG; 5.
DR   SMART; SM00136; LamNT; 1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; 12.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 13.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Laminin EGF-like domain.
SQ   SEQUENCE   3277 AA;  360209 MW;  3ACFFE998357122E CRC64;

  Query Match             76.2%;  Score 852;  DB 2;  Length 3277;
  Best Local Similarity   76.6%;  Pred. No. 4.5e-64;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       2682 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 2741

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| |||||:||||| ||  |||||| ||||||||:||||||
Db       2742 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGSPIFKSPQTYMDGLLHYVSVISDN 2801

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       2802 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 2861

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
               |:| |||||||||||||| |   |||| : | :|||
Db       2862 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 2899


RESULT 5
Q6VU68
ID   Q6VU68      PRELIMINARY;      PRT;  3333 AA.
AC   Q6VU68;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Laminin alpha 3 splice variant b1.
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
RA   McLean W.H., Irvine A.D., Hamill K.J., Whittock N.V.,
RA   Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
RA   Dopping-Hepenstal P.J., Eady R.A., Jamil T., Phillips R.J.,
RA   Shabbir S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
RA   Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
RA   McGrath J.A.;
RT   "An unusual N-terminal deletion of the laminin {alpha}3a isoform leads
RT   to the chronic granulation tissue disorder laryngo-onycho-cutaneous
RT   syndrome.";
RL   Hum. Mol. Genet. 12:2395-2409(2003).
RN   [2]
```

```
RP   SEQUENCE FROM N.A.
RA   McLean W.H.I.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY327115; AAQ72570.1; -.
DR   GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR   GO; GO:0005606; C:laminin-1; IEA.
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR008211; Laminin_N.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 8.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   Pfam; PF00055; Laminin_N; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   ProDom; PD003031; Laminin_B; 1.
DR   SMART; SM00181; EGF; 8.
DR   SMART; SM00180; EGF_Lam; 14.
DR   SMART; SM00281; LamB; 1.
DR   SMART; SM00282; LamG; 5.
DR   SMART; SM00136; LamNT; 1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; 12.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 13.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Laminin EGF-like domain.
SQ   SEQUENCE   3333 AA;  366646 MW;  9F99AF49B8EF27DD CRC64;

  Query Match             76.2%;  Score 852;  DB 2;  Length 3333;
  Best Local Similarity   76.6%;  Pred. No. 4.6e-64;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||:|||:| :| ||  | ||||
Db       2738 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 2797

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| |||||:||||| ||  |||||| |||||||:||||||
Db       2798 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGSPIFKSPQTYMDGLLHYVSVISDN 2857

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::|||||| :|||||||| ||| | ||||||| | |
Db       2858 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 2917

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
               |:| |||||||||||||| |   |||| : | :|||
Db       2918 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 2955


RESULT 6
LMA3_HUMAN
ID   LMA3_HUMAN     STANDARD;      PRT;  1713 AA.
AC   Q16787; Q13679; Q13680;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Laminin alpha-3 chain precursor (Epiligrin 170 kDa subunit) (E170)
DE   (Nicein alpha subunit).
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Keratinocytes;
RX   MEDLINE=94357926; PubMed=8077230;
RA   Ryan M.C., Tizard R., Vandevanter D.R., Carter W.G.;
RT   "Cloning of the LamA3 gene encoding the alpha 3 chain of the adhesive
RT   ligand epiligrin. Expression in wound repair.";
RL   J. Biol. Chem. 269:22779-22787(1994).
RN   [2]
RP   SEQUENCE OF 1-1331 FROM N.A. (ISOFORMS A AND B).
RX   MEDLINE=96163880; PubMed=8586427;
RA   Vidal F., Baudoin C., Miquel C., Galliano M.-F., Christiano A.M.,
RA   Uitto J., Ortonne J.-P., Meneguzzi G.;
RT   "Cloning of the laminin alpha 3 chain gene (LAMA3) and identification
RT   of a homozygous deletion in a patient with Herlitz junctional
RT   epidermolysis bullosa.";
RL   Genomics 30:273-280(1995).
RN   [3]
RP   DISEASE.
RX   PubMed=12915477; DOI=10.1093/hmg/ddg234;
RA   Irwin McLean W.H., Irvine A.D., Hamill K.J., Whittock N.V.,
RA   Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
RA   Dopping-Hepenstal P.J.H., Eady R.A.J., Jamil T., Phillips R.J.,
RA   Shabbir S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
RA   Darling J., Atherton D.J., Van Steensel M.A.M., Munro C.S.,
RA   Smith F.J.D., McGrath J.A.;
RT   "An unusual N-terminal deletion of the laminin alpha3a isoform leads
RT   to the chronic granulation tissue disorder laryngo-onycho-cutaneous
RT   syndrome.";
RL   Hum. Mol. Genet. 12:2395-2409(2003).
CC   -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC       is thought to mediate the attachment, migration and organization
CC       of cells into tissues during embryonic development by interacting
CC       with other extracellular matrix components.
CC   -!- FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
CC       via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-
CC       6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine
CC       phosphorylation of pp125-FAK and p80, (3) differentiation of
CC       keratinocytes.
CC   -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC       different polypeptide chains (alpha, beta, gamma), which are bound
CC       to each other by disulfide bonds into a cross-shaped molecule
CC       comprising one long and three short arms with globules at each
CC       end. The alpha-3 chain is a subunit of laminin-5
CC       (epiligrin/kalinin/nicein), and possibly also a component of
CC       laminin-6 (K-laminin) and laminin-7 (KS-laminin).
CC   -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC       membranes (major component).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=A;
CC         IsoId=Q16787-1; Sequence=Displayed;
CC       Name=B;
CC         IsoId=Q16787-2; Sequence=VSP_003037;
CC         Note=Incomplete sequence;
CC   -!- TISSUE SPECIFICITY: Skin; respiratory, urinary, and digestive
CC       epithelia and in other specialized tissues with prominent
CC       secretory or protective functions. Epithelial basement membrane,
CC       and epithelial cell tongue that migrates into a wound bed. A
CC       differential and focal expression of the alpha-3 chain is observed
CC       in the CNS.
CC   -!- INDUCTION: Laminin-5 is up-regulated in wound sites of human skin.
CC   -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC       with other laminin chains to form a coiled coil structure.
CC   -!- DOMAIN: Domain G is globular.
CC   -!- DISEASE: Defects in LAMA3 are a cause of junctional epidermolysis
CC       bullosa gravis (JEB) [MIM:226700]; also known as junctional
```

```
CC       epidermolysis bullosa Herlitz-Pearson type. JEB is a blistering
CC       disorder in skin that is characterized by a separation of basal
CC       cells from the basement membrane due to a decreased number of
CC       hemidesmosomes. Laminin-5 is missing from the basement membrane of
CC       patients with the gravis form of epidermolysis bullosa.
CC   -!- DISEASE: Defects in LAMA3 are the cause of laryngoonychocutaneous
CC       syndrome (LOCS) [MIM:245660]. LOCS is an autosomal recessive
CC       epithelial disorder confined to the Punjabi Muslim population. The
CC       condition is characterized by cutaneous erosions, nail dystrophy
CC       and exuberant vascular granulation tissue in certain epithelia,
CC       especially conjunctiva and larynx.
CC   -!- SIMILARITY: Contains 3 laminin EGF-like domains.
CC   -!- SIMILARITY: Contains 5 laminin G-like domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L34155; AAA59483.1; -.
DR   EMBL; X85107; CAA59428.1; -.
DR   EMBL; X85108; CAA59429.1; -.
DR   PIR; A55347; A55347.
DR   HSSP; P02468; 1NPE.
DR   Genew; HGNC:6483; LAMA3.
DR   MIM; 600805; -.
DR   MIM; 226700; -.
DR   MIM; 245660; -.
DR   GO; GO:0005604; C:basement membrane; TAS.
DR   GO; GO:0008544; P:epidermal differentiation; TAS.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00053; Laminin_EGF; 2.
DR   Pfam; PF00054; Laminin_G; 2.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Alternative splicing; Basement membrane; Cell adhesion; Coiled coil;
KW   Epidermolysis bullosa; Extracellular matrix; Glycoprotein;
KW   Laminin EGF-like domain; Repeat; Signal.
FT   SIGNAL       1     20       Potential.
FT   CHAIN       21   1713       Laminin alpha-3 chain.
FT   DOMAIN      46    201       Domain III A.
FT   DOMAIN      67    113       Laminin EGF-like 1.
FT   DOMAIN     114    166       Laminin EGF-like 2.
FT   DOMAIN     167    185       Laminin EGF-like 3 (incomplete).
FT   DOMAIN     186    769       Domain II and I.
FT   DOMAIN     770    971       Laminin G-like 1.
FT   DOMAIN     978   1140       Laminin G-like 2.
FT   DOMAIN    1147   1307       Laminin G-like 3.
FT   DOMAIN    1366   1530       Laminin G-like 4.
FT   DOMAIN    1537   1710       Laminin G-like 5.
FT   DOMAIN     231    327       Coiled coil (Potential).
FT   DOMAIN     396    548       Coiled coil (Potential).
FT   DOMAIN     594    621       Coiled coil (Potential).
FT   DOMAIN     702    765       Coiled coil (Potential).
FT   DOMAIN    1686   1713       Coiled coil (Potential).
FT   DISULFID    67     76       By similarity.
FT   DISULFID    69     83       By similarity.
FT   DISULFID    86     95       By similarity.
FT   DISULFID    98    111       By similarity.
FT   DISULFID   114    126       By similarity.
FT   DISULFID   116    135       By similarity.
FT   DISULFID   137    146       By similarity.
FT   DISULFID   149    164       By similarity.
FT   DISULFID   202    202       Interchain (Probable).
FT   DISULFID   205    205       Interchain (Probable).
FT   SITE       658    660       Cell attachment site (Potential).
FT   CARBOHYD   542    542       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   645    645       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   745    745       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   882    882       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   964    964       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1108   1108       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1131   1131       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1325   1325       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1477   1477       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD  1667   1667       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC     1     45       MGWLWIFGAALGQCLGYSSQQQRVPFLQPPGQSQLQASYVE
FT                               FRPS -> KVSSYGGYLTYQAKSFALPGDMVLLEKKPDVQL
FT                               TGQHMSIIYEETNTPRPDRLHHGRVHVVEGNFRHASSRAPV
FT                               SREELMTVLSRLADVRIQGLYFTETQRLTLSEVGLEEASDT
FT                               GSGRIALAVEICACPPAYAGDSC (in isoform B).
FT                               /FTId=VSP_003037.
FT   CONFLICT     5      5       W -> R (in Ref. 2).
FT   CONFLICT   123    125       ATG -> GMC (in Ref. 2).
FT   CONFLICT   481    481       M -> K (in Ref. 2).
FT   CONFLICT   754    754       R -> L (in Ref. 2).
FT   CONFLICT   969    969       E -> Q (in Ref. 2).
FT   CONFLICT  1052   1052       D -> A (in Ref. 2).
FT   CONFLICT  1184   1184       G -> A (in Ref. 2).
SQ   SEQUENCE  1713 AA;  189304 MW;  45EA9BE1017B60D3 CRC64;

  Query Match           76.0%;  Score 850;  DB 1;  Length 1713;
  Best Local Similarity  76.6%;  Pred. No. 3e-64;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASPSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1118 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1177

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| |||||||:||||| ||  |||||| |||||||:||||||
Db       1178 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1237

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              |||||||||:|| ::|| |:::|||||| :|||||||| ||| | ||||||| | |
Db       1238 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1297

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              |:| |||||||||||||| |   |||| : | :|||
Db       1298 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 7
Q96TG0
ID   Q96TG0      PRELIMINARY;      PRT;  1806 AA.
AC   Q96TG0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Alpha 3B chain of laminin-5 (Fragment).
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Aberdam D., Vidal, Baudoin, Miquel, Ortonne, Meneguzzi;
RL   Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X84900; CAA59325.1; -.
DR   HSSP; P02468; 1NPE.
DR   GO; GO:0005606; C:laminin-1; IEA.
```

```
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 2.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   ProDom; PD003031; Laminin_B; 1.
DR   SMART; SM00180; EGF_Lam; 2.
DR   SMART; SM00281; LamB; 1.
DR   SMART; SM00282; LamG; 5.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; 2.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Laminin EGF-like domain.
FT   NON_TER      1      1
SQ   SEQUENCE   1806 AA;  199411 MW;  EF94CDE2AEA52B93 CRC64;

  Query Match             76.0%;  Score 850;  DB 2;  Length 1806;
  Best Local Similarity   76.6%;  Pred. No. 3.2e-64;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:|||||||:|||:| :| ||  | ||||
Db       1211 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1270

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| ||||||:||||| ||  |||||| ||||||||:||||||
Db       1271 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1330

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1331 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1390

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
               |:| |||||||||||||| |   |||| : | :|||
Db       1391 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1428


RESULT 8
Q76E14
ID   Q76E14      PRELIMINARY;      PRT;  3333 AA.
AC   Q76E14;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Laminin alpha 3b chain.
GN   Name=LAMA3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kariya Y., Yasuda C., Nakashima Y., Ishida K., Tsubota Y.,
RA   Miyazaki K.;
RT   "Characterization of laminin 5B and NH2-terminal proteolytic fragment
RT   of its alpha3B chain: promotion of cellular adhesion, migration, and
RT   proliferation.";
RL   J. Biol. Chem. 279:24774-24784(2004).
DR   EMBL; AB107369; BAD13428.1; -.
DR   GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR   GO; GO:0005606; C:laminin-1; IEA.
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR008211; Laminin_N.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 8.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   Pfam; PF00055; Laminin_N; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   ProDom; PD003031; Laminin_B; 1.
DR   SMART; SM00181; EGF; 8.
DR   SMART; SM00180; EGF_Lam; 14.
DR   SMART; SM00281; LamB; 1.
DR   SMART; SM00282; LamG; 5.
DR   SMART; SM00136; LamNT; 1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; 12.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 13.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Laminin EGF-like domain.
SQ   SEQUENCE   3333 AA;  366616 MW;  6F99AF4D4B99FCB0 CRC64;

  Query Match             76.0%;  Score 850;  DB 2;  Length 3333;
  Best Local Similarity   76.6%;  Pred. No. 6.9e-64;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:|||||||:|||:| :| ||  | ||||
Db       2738 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 2797

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| ||||||:||||| ||  |||||| ||||||||:||||||
Db       2798 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 2857

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       2858 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 2917

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
               |:| |||||||||||||| |   |||| : | :|||
Db       2918 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 2955


RESULT 9
Q867A1
ID   Q867A1      PRELIMINARY;      PRT;  1725 AA.
AC   Q867A1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Laminin alpha 3 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Spirito F., Capt A., Guaguere E., Ortonne J.-P., Meneguzzi G.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF236865; AAL54876.1; -.
DR   HSSP; P11209; 1G2C.
DR   GO; GO:0005606; C:laminin-1; IEA.
DR   GO; GO:0005102; F:receptor binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR   GO; GO:0030334; P:regulation of cell migration; IEA.
DR   GO; GO:0045995; P:regulation of embryonic development; IEA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00053; Laminin_EGF; 2.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   SMART; SM00180; EGF_Lam; 2.
DR   SMART; SM00282; LamG; 5.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Laminin EGF-like domain.
FT   NON_TER    1725   1725
SQ   SEQUENCE   1725 AA;  191053 MW;  DF71EB0E1FB5134C CRC64;

  Query Match             68.0%;  Score 760.5;  DB 2;  Length 1725;
  Best Local Similarity   69.1%;  Pred. No. 1.6e-56;
  Matches  150;  Conservative   20;  Mismatches   46;  Indels    1;  Gaps    1;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              |||||||:||||||||||||||||||||||:||||| ||: || ||:|    || ||||
Db       1129 MKNLKKTTGVVRLNDTVGVTKKCSEDWKLVRSASFSRDGQLRFTGLDLPLPSEFQASFGF 1188

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| | | |:    | ||||||||||:||:::: | :|| ||||| || |||| |
Db       1189 QTFQPSGILFNLQSPKHYLQVTLEDGHIELNTRENSL-IIRSPQTYMDGELHFVSVIGDN 1247

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              |||||||||| |: ||:|    | :|  | |||  |||||||| :|| |:|| |||||||:
Db       1248 SGLRLLIDDQTLKSNQKLQDLSGSQHPLYLGGSQFEGCISNVFIQRVSKSPAVLDLASKT 1307

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQ 217
               |:| |||||||||||||| :   | ||   ||:||
Db       1308 FKRDVSLGGCSLNKPPFLMLLRGSTRLNKSHTFNINQ 1344


RESULT 10
Q91VV0
ID   Q91VV0      PRELIMINARY;      PRT;  1254 AA.
AC   Q91VV0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Lama4 protein (Fragment).
GN   Name=Lama4;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC008533; AAH08533.1; -.
DR   HSSP; Q60675; 1QU0.
DR   MGD; MGI:109321; Lama4.
DR   GO; GO:0005605; C:basal lamina; IDA.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0001568; P:blood vessel development; IMP.
DR   Pfam; PF02210; Laminin_G_2; 5.
DR   Pfam; PF06009; Laminin_II; 1.
DR   SMART; SM00282; LamG; 5.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
FT   NON_TER       1      1
SQ   SEQUENCE   1254 AA;  139723 MW;  54D49EF763D37CD9 CRC64;

  Query Match             18.2%;  Score 204;  DB 2;  Length 1254;
  Best Local Similarity   29.1%;  Pred. No. 1.3e-08;
  Matches   64;  Conservative   35;  Mismatches   99;  Indels   22;  Gaps    8;

Qy          5 KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD-VPSTDRFQLSFGFQTF 63
              ||   ::   :|:||   | ||  : | | |:  ||    ::  :   | |:  | |:|
Db        642 KKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIASIQKISFFDGFEGGFNFRTL 699

Qy         64 QPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHH-VSVISDTSG 122
              ||:| |  : : :    ::|::| : :  :   | :  :   | ||| |  |: ||||
Db        700 QPNGLLFYYTSGSDVFSISLDNGTVVMDVK--GIKVMSTDKQYHDGLPHFVVTSISDTR- 756

Qy        123 LRLLIDDQVLRRNQRLPSFSNAQQS------LRLGG-------GHFEGCISNVLVQRFSQ 169
               |::|   ||     |:   |:|:          ||         :| |||||   |  :
Db        757 YELVVDKSRLRGKN--PTKGKAEQTQTTEKKFYFGGSPISPQYANFTGCISNAYFTRLDR 814

Qy        170 SPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 209
               || |    | |   ||  | :   |  :| |  |  :|
Db        815 DVEVEDFQRYSEKVHTSLYECPIESSPLFLLHKKGKNSSK 854


RESULT 11
LMA4_MOUSE
ID   LMA4_MOUSE     STANDARD;      PRT;  1816 AA.
AC   P97927; O88785; P70409;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Laminin alpha-4 chain precursor.
GN   Name=Lama4;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
```

```
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 462-469; 478-483; 776-782 AND
RP   940-945.
RC   STRAIN=BALB/c; TISSUE=Endothelial cells;
RX   MEDLINE=97363207; PubMed=9219532;
RA   Frieser M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,
RA   Sorokin L.M.;
RT   "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of
RT   endothelium.";
RL   Eur. J. Biochem. 246:727-735(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=97202462; PubMed=9049981; DOI=10.1016/S0945-053X(96)90162-6;
RA   Liu J., Mayne R.;
RT   "The complete cDNA coding sequence and tissue-specific expression of
RT   the mouse laminin alpha 4 chain.";
RL   Matrix Biol. 15:433-437(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=98010627; PubMed=9346933; DOI=10.1074/jbc.272.44.27862;
RA   Iivanainen A., Kortesmaa J., Sahlberg C., Morita T., Bergmann U.,
RA   Thesleff I., Tryggvason K.;
RT   "Primary structure, developmental expression, and immunolocalization
RT   of the murine laminin alpha4 chain.";
RL   J. Biol. Chem. 272:27862-27868(1997).
RN   [4]
RP   SEQUENCE OF 836-1106 FROM N.A.
RC   STRAIN=ICR; TISSUE=Placenta;
RX   MEDLINE=97296337; PubMed=9151674; DOI=10.1083/jcb.137.3.685;
RA   Miner J.H., Patton B.L., Lentz S.I., Gilbert D.J., Snider W.D.,
RA   Jenkins N.A., Copeland N.G., Sanes J.R.;
RT   "The laminin alpha chains: expression, developmental transitions, and
RT   chromosomal locations of alpha1-5, identification of heterotrimeric
RT   laminins 8-11, and cloning of a novel alpha3 isoform.";
RL   J. Cell Biol. 137:685-702(1997).
RN   [5]
RP   SEQUENCE OF 1467-1691 FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=97187457; PubMed=9034910;
RX   DOI=10.1002/(SICI)1096-9861(19970224)378:4<547::AID-CNE9>3.0.CO;2-2;
RA   Lentz S.I., Miner J.H., Sanes J.R., Snider W.D.;
RT   "Distribution of the ten known laminin chains in the pathways and
RT   targets of developing sensory axons.";
RL   J. Comp. Neurol. 378:547-561(1997).
CC   -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC       is thought to mediate the attachment, migration and organization
CC       of cells into tissues during embryonic development by interacting
CC       with other extracellular matrix components.
CC   -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC       different polypeptide chains (alpha, beta, gamma), which are bound
CC       to each other by disulfide bonds into a cross-shaped molecule
CC       comprising one long and three short arms with globules at each
CC       end.
CC   -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC       membranes (major component).
CC   -!- TISSUE SPECIFICITY: Strongly expressed in peripheral nerves,
CC       cardiac muscle, fat, dermis, lung stroma, aortic endothelium,
CC       endocardium and endothelium of blood vessels in skin and brain.
CC   -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC       with other laminin chains to form a coiled coil structure.
CC   -!- DOMAIN: Domain G is globular.
CC   -!- SIMILARITY: Contains 4 laminin EGF-like domains.
CC   -!- SIMILARITY: Contains 5 laminin G-like domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U58950; AAB41840.1; -.
DR   EMBL; Y09827; CAA70970.1; -.
DR   EMBL; U59865; AAC24725.1; -.
DR   EMBL; U88352; AAC53178.1; -.
DR   EMBL; U69176; AAC52982.1; -.
DR   HSSP; P02468; 1NPE.
DR   MGD; MGI:109321; Lama4.
DR   GO; GO:0005604; C:basement membrane; IDA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00053; Laminin_EGF; 3.
DR   Pfam; PF00054; Laminin_G; 4.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Basement membrane; Cell adhesion; Coiled coil;
KW   Direct protein sequencing; Extracellular matrix; Glycoprotein;
KW   Laminin EGF-like domain; Repeat; Signal.
FT   SIGNAL        1     24       Potential.
FT   CHAIN        25   1816       Laminin alpha-4 chain.
FT   DOMAIN       82    131       Laminin EGF-like 1.
FT   DOMAIN      132    186       Laminin EGF-like 2.
FT   DOMAIN      187    240       Laminin EGF-like 3.
FT   DOMAIN      241    255       Laminin EGF-like 4 (incomplete).
FT   DOMAIN      256    825       Domain II and I.
FT   DOMAIN      826   1030       Laminin G-like 1.
FT   DOMAIN     1042   1222       Laminin G-like 2.
FT   DOMAIN     1229   1397       Laminin G-like 3.
FT   DOMAIN     1462   1633       Laminin G-like 4.
FT   DOMAIN     1640   1813       Laminin G-like 5.
FT   DOMAIN      431    523       Coiled coil (Potential).
FT   DOMAIN      556    604       Coiled coil (Potential).
FT   DOMAIN      655    717       Coiled coil (Potential).
FT   DOMAIN      770    799       Coiled coil (Potential).
FT   SITE        717    719       Cell attachment site (Potential).
FT   DISULFID     82     91       By similarity.
FT   DISULFID     84     98       By similarity.
FT   DISULFID    101    110       By similarity.
FT   DISULFID    113    129       By similarity.
FT   DISULFID    132    146       By similarity.
FT   DISULFID    134    155       By similarity.
FT   DISULFID    157    166       By similarity.
FT   DISULFID    169    184       By similarity.
FT   DISULFID    187    202       By similarity.
FT   DISULFID    189    209       By similarity.
FT   DISULFID    212    221       By similarity.
FT   DISULFID    224    238       By similarity.
FT   DISULFID    266    266       Interchain (Probable).
FT   DISULFID    269    269       Interchain (Probable).
FT   CARBOHYD    104    104       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    215    215       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    308    308       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    333    333       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    458    458       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    550    550       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    571    571       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    574    574       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    631    631       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    639    639       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    735    735       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    751    751       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    754    754       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    780    780       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    803    803       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1088   1088       N-linked (GlcNAc. . .) (Potential).
```

```
FT   CARBOHYD   1283   1283       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1361   1361       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT      8      8       C -> S (in Ref. 2).
FT   CONFLICT     18     18       C -> Y (in Ref. 2).
FT   CONFLICT    248    248       C -> R (in Ref. 3).
FT   CONFLICT    297    297       G -> A (in Ref. 3).
FT   CONFLICT    431    433       THR -> HPS (in Ref. 2).
FT   CONFLICT    679    679       S -> C (in Ref. 3).
FT   CONFLICT    703    703       D -> G (in Ref. 2).
FT   CONFLICT    706    706       N -> H (in Ref. 2).
FT   CONFLICT    728    728       K -> R (in Ref. 2).
FT   CONFLICT    730    730       F -> I (in Ref. 2).
FT   CONFLICT    779    779       R -> G (in Ref. 1; AA sequence).
FT   CONFLICT    810    810       R -> S (in Ref. 3).
FT   CONFLICT    865    867       AEP -> QT (in Ref. 2).
FT   CONFLICT    936    936       K -> E (in Ref. 3).
FT   CONFLICT    970    970       L -> V (in Ref. 3).
FT   CONFLICT   1132   1132       H -> R (in Ref. 2).
FT   CONFLICT   1200   1200       F -> I (in Ref. 2).
FT   CONFLICT   1382   1382       D -> A (in Ref. 2).
FT   CONFLICT   1413   1414       NS -> EF (in Ref. 1).
FT   CONFLICT   1489   1489       A -> S (in Ref. 2).
SQ   SEQUENCE   1816 AA;  201818 MW;  B49C45F3A45999D8 CRC64;

  Query Match             18.2%;  Score 204;  DB 1;  Length 1816;
  Best Local Similarity   29.1%;  Pred. No. 2e-08;
  Matches   64;  Conservative   35;  Mismatches   99;  Indels   22;  Gaps    8;

Qy          5 KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD-VPSTDRFQLSFGFQTF 63
              ||   ::   :|:||   | ||  : | | |:  ||    ::  :   | |:  | |:|
Db       1204 KKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIASIQKISFFDGFEGGFNFRTL 1261

Qy         64 QPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHH-VSVISDTSG 122
              ||:| |  : : :    ::|::| : :  :   | :  :   | ||| |  |: ||||
Db       1262 QPNGLLFYYTSGSDVFSISLDNGTVVMDVK--GIKVMSTDKQYHDGLPHFVVTSISDTR- 1318

Qy        123 LRLLIDDQVLRRNQRLPSFSNAQQS------LRLGG-------GHFEGCISNVLVQRFSQ 169
               |::|   ||     |:   |:|:        ||        :| |||||    |  :
Db       1319 YELVVDKSRLRGKN--PTKGKAEQTQTTEKKFYFGGSPISPQYANFTGCISNAYFTRLDR 1376

Qy        170 SPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 209
               || |    | |   ||  | :   |  :| |  |  :|
Db       1377 DVEVEDFQRYSEKVHTSLYECPIESSPLFLLHKKGKNSSK 1416


RESULT 12
LMA4_HUMAN
ID   LMA4_HUMAN     STANDARD;      PRT;  1816 AA.
AC   Q16363; Q14735; Q15335; Q9UE18; Q9UJN9;
DT   01-NOV-1997 (Rel. 35, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Laminin alpha-4 chain precursor.
GN   Name=LAMA4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal lung;
RX   MEDLINE=95300971; PubMed=7781776; DOI=10.1016/0014-5793(95)00462-I;
RA   Iivanainen A., Sainio K., Sariola H., Tryggvason K.;
RT   "Primary structure and expression of a novel human laminin alpha 4
RT   chain.";
RL   FEBS Lett. 365:183-188(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=97454279; PubMed=9310354;
RA   Richards A.J., Luccarini C., Pope F.M.;
RT   "The structural organisation of LAMA4, the gene encoding laminin
RT   alpha4.";
RL   Eur. J. Biochem. 248:15-23(1997).
RN   [3]
RP   SEQUENCE OF 236-1816 FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=95048381; PubMed=7959779;
RA   Richards A.J., Al-Imara L., Carter N.P., Lloyd J.C., Leversha M.A.,
RA   Pope F.M.;
RT   "Localization of the gene (LAMA4) to chromosome 6q21 and isolation of
RT   a partial cDNA encoding a variant laminin A chain.";
RL   Genomics 22:237-239(1994).
RN   [4]
RP   SEQUENCE OF 66-1816 FROM N.A.
RA   Tubby B.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC       is thought to mediate the attachment, migration and organization
CC       of cells into tissues during embryonic development by interacting
CC       with other extracellular matrix components.
CC   -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC       different polypeptide chains (alpha, beta, gamma), which are bound
CC       to each other by disulfide bonds into a cross-shaped molecule
CC       comprising one long and three short arms with globules at each
CC       end.
CC   -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC       membranes (major component).
CC   -!- TISSUE SPECIFICITY: In adult, strong expression in heart, lung,
CC       ovary small and large intestines, placenta, liver; weak or no
CC       expression in skeletal muscle, kidney, pancreas, testis, prostate,
CC       brain. High expression in fetal lung and kidney. Expression in
CC       fetal and newborn tissues is observed in certain mesenchymal cells
CC       in tissues such as smooth muscle and dermis.
CC   -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC       with other laminin chains to form a coiled coil structure.
CC   -!- DOMAIN: Domain G is globular.
CC   -!- SIMILARITY: Contains 4 laminin EGF-like domains.
CC   -!- SIMILARITY: Contains 5 laminin G-like domains.
CC   -!- CAUTION: Gene LAMA4 was formerly called LAMA3.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S78569; AAB34635.1; -.
DR   EMBL; X91171; CAA62596.1; -.
DR   EMBL; Y14240; CAA74636.1; -.
DR   EMBL; X76939; CAA54258.1; -.
DR   EMBL; Z99289; -; NOT_ANNOTATED_CDS.
DR   PIR; S68960; S68960.
DR   HSSP; P02468; 1NPE.
DR   Genew; HGNC:6484; LAMA4.
DR   MIM; 600133; -.
DR   GO; GO:0005605; C:basal lamina; TAS.
DR   GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00053; Laminin_EGF; 3.
DR   Pfam; PF00054; Laminin_G; 3.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
KW   Basement membrane; Cell adhesion; Coiled coil; Extracellular matrix;
KW   Glycoprotein; Laminin EGF-like domain; Repeat; Signal.
```

```
FT   SIGNAL       1     24       Potential.
FT   CHAIN        25   1816       Laminin alpha-4 chain.
FT   DOMAIN       82    131       Laminin EGF-like 1.
FT   DOMAIN      132    186       Laminin EGF-like 2.
FT   DOMAIN      187    240       Laminin EGF-like 3.
FT   DOMAIN      241    255       Laminin EGF-like 4 (incomplete).
FT   DOMAIN      256    825       Domain II and I.
FT   DOMAIN      826   1028       Laminin G-like 1.
FT   DOMAIN     1040   1220       Laminin G-like 2.
FT   DOMAIN     1227   1395       Laminin G-like 3.
FT   DOMAIN     1462   1633       Laminin G-like 4.
FT   DOMAIN     1640   1813       Laminin G-like 5.
FT   DOMAIN      313    396       Coiled coil (Potential).
FT   DOMAIN      466    521       Coiled coil (Potential).
FT   DOMAIN      574    607       Coiled coil (Potential).
FT   DOMAIN      655    717       Coiled coil (Potential).
FT   DOMAIN      770    799       Coiled coil (Potential).
FT   SITE        717    719       Cell attachment site (Potential).
FT   DISULFID     82     91       By similarity.
FT   DISULFID     84     98       By similarity.
FT   DISULFID    101    110       By similarity.
FT   DISULFID    113    129       By similarity.
FT   DISULFID    132    146       By similarity.
FT   DISULFID    134    155       By similarity.
FT   DISULFID    157    166       By similarity.
FT   DISULFID    169    184       By similarity.
FT   DISULFID    187    202       By similarity.
FT   DISULFID    189    209       By similarity.
FT   DISULFID    212    221       By similarity.
FT   DISULFID    224    238       By similarity.
FT   DISULFID    266    266       Interchain (Probable).
FT   DISULFID    269    269       Interchain (Probable).
FT   CARBOHYD    104    104       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    215    215       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    308    308       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    458    458       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    524    524       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    550    550       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    571    571       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    574    574       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    631    631       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    639    639       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    735    735       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    751    751       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    754    754       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    780    780       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    803    803       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1086   1086       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1281   1281       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1359   1359       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1411   1411       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT    143    143       A -> P (in Ref. 1).
FT   CONFLICT    178    178       L -> F (in Ref. 1).
FT   CONFLICT    265    265       G -> GMDCPTIS (in Ref. 4).
FT   CONFLICT    276    276       D -> A (in Ref. 4).
FT   CONFLICT    491    491       Y -> H (in Ref. 2 and 3).
FT   CONFLICT   1057   1057       T -> P (in Ref. 1).
FT   CONFLICT   1110   1112       SGR -> GGP (in Ref. 4).
SQ   SEQUENCE   1816 AA;  201908 MW;  04E9AF379A0F4A4D CRC64;

  Query Match             16.7%;  Score 187;  DB 1;  Length 1816;
  Best Local Similarity   28.3%;  Pred. No. 6e-07;
  Matches   62;  Conservative   34;  Mismatches  103;  Indels   20;  Gaps    8;

Qy          5 KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD-VPSTDRFQLSFGFQTF 63
              ||   ::   :|:||   | ||  : | | |: ||    ::  :   | |:  | |:||
Db       1202 KKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIASIQKISFFDGFEGGFNFRTL 1259

Qy         64 QPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGL 123
              ||:| |  : : :    ::|::| : :  :   | :      | ||| |   |||  |
Db       1260 QPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQSVDKQYNDGLSHF--VISSVSPT 1315

Qy        124 R--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-------GHFEGCISNVLVQRFSQS 170
                 |  |::|  :|  :|         | | :   ||        :| |||||    | :
Db       1316 RYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSPISAQYANFTGCISNAYFTRVDRD 1375

Qy        171 PEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 209
              || |    : |   ||  | :   |  :| | |  :|
Db       1376 VEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNLSK 1414


RESULT 13
Q8R3Y7
ID   Q8R3Y7      PRELIMINARY;      PRT;   794 AA.
AC   Q8R3Y7;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Lama5 protein (Fragment).
GN   Name=Lama5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020313; AAH20313.1; -.
DR   HSSP; Q14393; 1H30.
DR   MGD; MGI:105382; Lama5.
DR   GO; GO:0005604; C:basement membrane; IDA.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005178; F:integrin binding; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0001763; P:branching morphogenesis; IDA.
DR   GO; GO:0030324; P:lung development; IMP.
DR   GO; GO:0007517; P:muscle development; IMP.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF02210; Laminin_G_2; 4.
DR   SMART; SM00282; LamG; 4.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 4.
FT   NON_TER      1      1
SQ   SEQUENCE   794 AA;  86936 MW;  5316391F38E5682C CRC64;

  Query Match             16.6%;  Score 186;  DB 2;  Length 794;
  Best Local Similarity   29.2%;  Pred. No. 2.6e-07;
  Matches   59;  Conservative   34;  Mismatches   91;  Indels   18;  Gaps    6;
```

```
Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDV-PSTDRFQLSFG 59
              :| | |    : ||| | |::  |: |  : || :|   | :      || | |:     ||
Db        174 IKALGKYVDLKRLN-TTGISFGCTADLLVGRTMTFHGHGFLPLALPDVAPITEVVYSGFG 232

Qy         60 FQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISD 119
              |:  | :  |     :      |:| :||: |   :  :   ::   : ||  |:|:  |:
Db        233 FRGTQDNNLLYYRTSPDGPYQVSLREGHVTLRFMNQEV---ETQRVFADGAPHYVAFYSN 289

Qy        120 TSGLRLLLIDD--QVLRRNQRLPSFSNAQ----QSLRLGG-------GHFEGCISNVLVQR 166
               :|: | :||  |::: ::|       |       | |||           :| |||||| |||
Db        290 VTGVWLYVDDQLQLVKSHERTTPMLQLQPEEPSRLLLGGLPVSGTFHNFSGCISNVFVQR 349

Qy        167 FSQSPEVLDLASKSTKKDASLG 188
                  | ||       : |:|
Db        350 LRGPQRVFDLHQNMGSVNVSVG 371
```

RESULT 14
Q6ZQA1
ID Q6ZQA1 PRELIMINARY; PRT; 1524 AA.
AC Q6ZQA1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MKIAA0533 protein (Fragment).
GN Name=mKIAA0533;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic tail;
RX PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129157; BAC97967.2; -.
DR GO; GO:0005604; C:basement membrane; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005178; F:integrin binding; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0001763; P:branching morphogenesis; IDA.
DR GO; GO:0030324; P:lung development; IMP.
DR GO; GO:0007517; P:muscle development; IMP.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR001368; TNFR_c6.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00053; Laminin_EGF; 2.
DR Pfam; PF02210; Laminin_G_2; 4.
DR Pfam; PF06008; Laminin_I; 1.
DR Pfam; PF06009; Laminin_II; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR SMART; SM00180; EGF_Lam; 2.
DR SMART; SM00282; LamG; 5.
DR PROSITE; PS00022; EGF_1; UNKNOWN_3.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
KW Laminin EGF-like domain.
FT NON_TER 1 1
FT NON_TER 1524 1524
SQ SEQUENCE 1524 AA; 166516 MW; F43411828FF8E691 CRC64;

```
  Query Match             16.6%;  Score 186;  DB 2;  Length 1524;
  Best Local Similarity   29.2%;  Pred. No. 5.8e-07;
  Matches   59;  Conservative   34;  Mismatches   91;  Indels   18;  Gaps    6;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDV-PSTDRFQLSFG 59
              :| | |    : ||| | |::  |: |  : || :|   | :      || | |:     ||
Db        931 IKALGKYVDLKRLN-TTGISFGCTADLLVGRTMTFHGHGFLPLALPDVAPITEVVYSGFG 989

Qy         60 FQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISD 119
              |:  | :  |     :      |:| :||: |   :  :   ::   : ||  |:|:  |:
Db        990 FRGTQDNNLLYYRTSPDGPYQVSLREGHVTLRFMNQEV---ETQRVFADGAPHYVAFYSN 1046

Qy        120 TSGLRLLLIDD--QVLRRNQRLPSFSNAQ----QSLRLGG-------GHFEGCISNVLVQR 166
               :|: | :||  |::: ::|       |       | |||           :| |||||| |||
Db       1047 VTGVWLYVDDQLQLVKSHERTTPMLQLQPEEPSRLLLGGLPVSGTFHNFSGCISNVFVQR 1106

Qy        167 FSQSPEVLDLASKSTKKDASLG 188
                  | ||       : |:|
Db       1107 LRGPQRVFDLHQNMGSVNVSVG 1128
```

RESULT 15
LMA5_MOUSE
ID LMA5_MOUSE STANDARD; PRT; 3718 AA.
AC Q61001; Q9JHQ6;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Laminin alpha-5 chain precursor.
GN Name=Lama5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-92 FROM N.A., AND SEQUENCE OF 41-46.
RX MEDLINE=21818471; PubMed=11829758; DOI=10.1042/0264-6021:3620213;
RA Garbe J.H., Gohring W., Mann K., Timpl R., Sasaki T.;
RT "Complete sequence, recombinant analysis and binding to laminins and
RT sulphated ligands of the N-terminal domains of laminin alpha3B and
RT alpha5 chains.";
RL Biochem. J. 362:213-221(2002).
RN [2]
RP SEQUENCE OF 84-3718 FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Lung;
RX MEDLINE=96081906; PubMed=7499364; DOI=10.1074/jbc.270.48.28523;
RA Miner J.H., Lewis R.M., Sanes J.R.;
RT "Molecular cloning of a novel laminin chain, alpha 5, and widespread
RT expression in adult mouse tissues.";
RL J. Biol. Chem. 270:28523-28526(1995).
RN [3]
RP REVISIONS.
RA Miner J.H., Lewis R.M., Sanes J.R.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components. Alpha-5 chain may be
CC the major laminin alpha chain of adult epithelial and/or
CC endothelial basal laminae.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end.
CC -!- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC membranes (major component).
CC -!- TISSUE SPECIFICITY: In adult, high levels in heart, lung, and
CC kidney; lower in brain, muscle and testis; very low in liver, gut
CC and skin. Expressed in many tissues in embryonic day 11.
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.

```
CC   -!- DOMAIN: Domains VI, IV and G are globular.
CC   -!- SIMILARITY: Contains 22 laminin EGF-like domains.
CC   -!- SIMILARITY: Contains 5 laminin G-like domains.
CC   -!- SIMILARITY: Contains 2 laminin IV domains.
CC   -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ293593; CAB99255.1; -.
DR   EMBL; U37501; AAC53430.1; -.
DR   PIR; T10053; T10053.
DR   HSSP; P02468; 1NPE.
DR   MGD; MGI:105382; Lama5.
DR   GO; GO:0005604; C:basement membrane; IDA.
DR   GO; GO:0005178; F:integrin binding; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0001763; P:branching morphogenesis; IDA.
DR   GO; GO:0030324; P:lung development; IMP.
DR   GO; GO:0007517; P:muscle development; IMP.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR009254; Laminin_I.
DR   InterPro; IPR010307; Laminin_II.
DR   InterPro; IPR008211; Laminin_N.
DR   InterPro; IPR008212; Lam_N2.
DR   InterPro; IPR003129; TSP_N.
DR   Pfam; PF00052; Laminin_B; 1.
DR   Pfam; PF00053; Laminin_EGF; 17.
DR   Pfam; PF00054; Laminin_G; 2.
DR   Pfam; PF06008; Laminin_I; 1.
DR   Pfam; PF06009; Laminin_II; 1.
DR   Pfam; PF00055; Laminin_N; 1.
DR   PRINTS; PR00011; EGFLAMININ.
DR   ProDom; PD003031; Laminin_B; 1.
DR   PROSITE; PS00022; EGF_1; 19.
DR   PROSITE; PS01186; EGF_2; 3.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW   Basement membrane; Cell adhesion; Coiled coil;
KW   Direct protein sequencing; Extracellular matrix; Glycoprotein;
KW   Laminin EGF-like domain; Repeat; Signal.
FT   SIGNAL        1     40
FT   CHAIN        41   3718       Laminin alpha-5 chain.
FT   DOMAIN       41    304       Laminin N-terminal (domain VI).
FT   DOMAIN      305    363       Laminin EGF-like 1.
FT   DOMAIN      364    433       Laminin EGF-like 2.
FT   DOMAIN      434    479       Laminin EGF-like 3.
FT   DOMAIN      500    546       Laminin EGF-like 4.
FT   DOMAIN      547    592       Laminin EGF-like 5.
FT   DOMAIN      593    637       Laminin EGF-like 6.
FT   DOMAIN      638    682       Laminin EGF-like 7.
FT   DOMAIN      683    728       Laminin EGF-like 8.
FT   DOMAIN      729    781       Laminin EGF-like 9.
FT   DOMAIN      782    833       Laminin EGF-like 10.
FT   DOMAIN      834    855       Laminin EGF-like 11 (incomplete).
FT   DOMAIN      856   1442       Laminin domain IV 1 (domain IV B).
FT   DOMAIN     1443   1488       Laminin EGF-like 12.
FT   DOMAIN     1489   1532       Laminin EGF-like 13.
FT   DOMAIN     1533   1581       Laminin EGF-like 14.
FT   DOMAIN     1582   1632       Laminin EGF-like 15.
FT   DOMAIN     1633   1642       Laminin EGF-like 16 (N-terminal).
FT   DOMAIN     1643   1831       Laminin domain IV 2 (domain IV A).
FT   DOMAIN     1832   1864       Laminin EGF-like 16 (C-terminal).
FT   DOMAIN     1865   1914       Laminin EGF-like 17.
FT   DOMAIN     1915   1970       Laminin EGF-like 18.
FT   DOMAIN     1971   2024       Laminin EGF-like 19.
FT   DOMAIN     2025   2071       Laminin EGF-like 20.
FT   DOMAIN     2072   2118       Laminin EGF-like 21.
FT   DOMAIN     2119   2168       Laminin EGF-like 22.
FT   DOMAIN     2169   2735       Domain II and I.
FT   DOMAIN     2736   2933       Laminin G-like 1.
FT   DOMAIN     2947   3119       Laminin G-like 2.
FT   DOMAIN     3128   3296       Laminin G-like 3.
FT   DOMAIN     3337   3511       Laminin G-like 4.
FT   DOMAIN     3518   3689       Laminin G-like 5.
FT   DOMAIN     2205   2257       Coiled coil (Potential).
FT   DOMAIN     2330   2464       Coiled coil (Potential).
FT   DOMAIN     2604   2621       Coiled coil (Potential).
FT   DOMAIN     2639   2705       Coiled coil (Potential).
FT   SITE       1723   1725       Cell attachment site (Potential).
FT   SITE       1839   1841       Cell attachment site (Potential).
FT   DISULFID    305    314       By similarity.
FT   DISULFID    307    327       By similarity.
FT   DISULFID    329    338       By similarity.
FT   DISULFID    341    361       By similarity.
FT   DISULFID    364    373       By similarity.
FT   DISULFID    366    398       By similarity.
FT   DISULFID    401    410       By similarity.
FT   DISULFID    413    431       By similarity.
FT   DISULFID    434    445       By similarity.
FT   DISULFID    436    452       By similarity.
FT   DISULFID    454    463       By similarity.
FT   DISULFID    466    476       By similarity.
FT   DISULFID    500    512       By similarity.
FT   DISULFID    502    521       By similarity.
FT   DISULFID    523    532       By similarity.
FT   DISULFID    535    544       By similarity.
FT   DISULFID    547    559       By similarity.
FT   DISULFID    549    566       By similarity.
FT   DISULFID    568    577       By similarity.
FT   DISULFID    580    590       By similarity.
FT   DISULFID    593    605       By similarity.
FT   DISULFID    595    611       By similarity.
FT   DISULFID    613    622       By similarity.
FT   DISULFID    625    635       By similarity.
FT   DISULFID    638    650       By similarity.
FT   DISULFID    640    656       By similarity.
FT   DISULFID    658    667       By similarity.
FT   DISULFID    670    680       By similarity.
FT   DISULFID    683    695       By similarity.
FT   DISULFID    685    702       By similarity.
FT   DISULFID    704    713       By similarity.
FT   DISULFID    716    726       By similarity.
FT   DISULFID   1443   1455       By similarity.
FT   DISULFID   1445   1462       By similarity.
FT   DISULFID   1464   1473       By similarity.
FT   DISULFID   1476   1486       By similarity.
FT   DISULFID   1533   1548       By similarity.
FT   DISULFID   1535   1555       By similarity.
FT   DISULFID   1557   1566       By similarity.
FT   DISULFID   1569   1579       By similarity.
FT   DISULFID   1582   1594       By similarity.
FT   DISULFID   1584   1601       By similarity.
FT   DISULFID   1603   1612       By similarity.
FT   DISULFID   1615   1630       By similarity.
FT   DISULFID   1865   1874       By similarity.
FT   DISULFID   1867   1881       By similarity.
FT   DISULFID   1884   1893       By similarity.
FT   DISULFID   1896   1912       By similarity.
FT   DISULFID   1915   1930       By similarity.
FT   DISULFID   1917   1939       By similarity.
FT   DISULFID   1941   1950       By similarity.
FT   DISULFID   1953   1968       By similarity.
FT   DISULFID   1971   1986       By similarity.
FT   DISULFID   1973   1993       By similarity.
```

```
FT   DISULFID   1996   2005       By similarity.
FT   DISULFID   2008   2022       By similarity.
FT   DISULFID   2072   2083       By similarity.
FT   DISULFID   2074   2090       By similarity.
FT   DISULFID   2092   2101       By similarity.

  Query Match             16.6%;  Score 186;  DB 1;  Length 3718;
  Best Local Similarity   29.2%;  Pred. No. 1.8e-06;
  Matches   59;  Conservative   34;  Mismatches   91;  Indels   18;  Gaps    6;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDV-PSTDRFQLSFG 59
              :| | |   : ||| | |::  |: |  : || :|   | :     || | |:     ||
Db       3098 IKALGKYVDLKRLN-TTGISFGCTADLLVGRTMTFHGHGFLPLALPDVAPITEVVYSGFG 3156

Qy         60 FQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISD 119
              |:  | :  |    :       |:| :||: |   :  :   ::   : ||  |:|:  |:
Db       3157 FRGTQDNNLLYYRTSPDGPYQVSLREGHVTLRFMNQEV---ETQRVFADGAPHYVAFYSN 3213

Qy        120 TSGLRLLIDD--QVLRRNQRLPSFSNAQ----QSLRLGG-------GHFEGCISNVLVQR 166
               :|: | :||  |::: ::|       |      | |||         :| |||||| |||
Db       3214 VTGVWLYVDDQLQLVKSHERTTPMLQLQPEEPSRLLLGGLPVSGTFHNFSGCISNVFVQR 3273

Qy        167 FSQSPEVLDLASKSTKKDASLG 188
                 | ||       : |:|
Db       3274 LRGPQRVFDLHQNMGSVNVSVG 3295


Search completed: February 22, 2005, 08:24:24
Job time : 37.8842 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:04:10 ; Search time 40.1892 Seconds
(without alignments)
2097.921 Million cell updates/sec

Title: US-10-817-423-6
Perfect score: 1118
Sequence: 1 MKNLKKTSGVVRLNDTVGVT.....MLFKSPKRFNKGRIFNVNQL 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1118	100.0	1694	3	AAB48461	Aab48461 Rat lamin
2	1118	100.0	1725	3	AAB48460	Aab48460 Rat lamin
3	850	76.0	1693	3	AAB48459	Aab48459 Human lam
4	850	76.0	1693	3	AAB48457	Aab48457 Human lam
5	850	76.0	1713	2	AAR70148	Aar70148 Deduced s
6	850	76.0	1713	3	AAB48458	Aab48458 Human lam
7	850	76.0	1713	6	ABR92102	Abr92102 Human cer
8	850	76.0	1713	7	ADD29904	Add29904 Human lam
9	850	76.0	1713	7	ADG37225	Adg37225 Human lam
10	850	76.0	1713	8	ABM81957	Abm81957 Tumour-as
11	850	76.0	1713	8	ADR87606	Adr87606 Human Lam
12	850	76.0	1724	3	AAB48456	Aab48456 Human lam
13	850	76.0	3332	7	ADE08094	Ade08094 Novel pro
14	680	60.8	469	4	AAG75103	Aag75103 Human col
15	204	18.2	1792	3	AAB48447	Aab48447 Mouse lam
16	204	18.2	1816	3	AAB48446	Aab48446 Mouse lam
17	196.5	17.6	983	5	ABB80818	Abb80818 Heparin b
18	196.5	17.6	1815	5	ABB80853	Abb80853 Heparin b
19	187	16.7	984	5	ABB80819	Abb80819 Heparin b
20	187	16.7	1581	7	ADJ68348	Adj68348 Human hea
21	187	16.7	1792	3	AAB48443	Aab48443 Human lam
22	187	16.7	1800	3	AAB48445	Aab48445 Human lam
23	187	16.7	1816	3	AAB48442	Aab48442 Human lam
24	187	16.7	1816	7	ADC01877	Adc01877 Human lam
25	187	16.7	1816	7	ADC01879	Adc01879 Human lam
26	187	16.7	1816	8	ADP08401	Adp08401 Human lam
27	187	16.7	1816	8	ADR87600	Adr87600 Human Lam
28	187	16.7	1823	5	ABP63020	Abp63020 Human pol
29	187	16.7	1824	3	AAB48444	Aab48444 Human lam
30	186	16.6	3635	5	ABB81589	Abb81589 Mouse lam
31	186	16.6	3635	5	AAM50357	Aam50357 Mouse lam
32	186	16.6	3635	8	ADP74034	Adp74034 Murine la
33	177	15.8	3597	8	ADO10047	Ado10047 Novel hum
34	176	15.7	3597	5	ABB09503	Abb09503 Human lam
35	176	15.7	3600	5	ABB09501	Abb09501 Human lam
36	176	15.7	3690	8	ADM87254	Adm87254 Human pro
37	175	15.7	49	3	AAB53609	Aab53609 Human col
38	174	15.6	463	5	ABP41907	Abp41907 Human ova
39	174	15.6	908	5	ABB09502	Abb09502 Human lam
40	174	15.6	953	5	AAM50358	Aam50358 Human lam
41	174	15.6	1601	4	AAM39009	Aam39009 Human pol
42	174	15.6	1640	5	ABB09504	Abb09504 Human lam
43	174	15.6	1640	8	ADO10049	Ado10049 Novel hum
44	174	15.6	1645	7	ADL15098	Adl15098 Human mal
45	174	15.6	1645	7	ADN95658	Adn95658 Human BEC

ALIGNMENTS

RESULT 1
AAB48461
ID AAB48461 standard; protein; 1694 AA.
XX
AC AAB48461;
XX
DT 02-MAR-2001 (first entry)
XX
DE Rat laminin 5 polypeptide, SEQ ID NO: 12.
XX
KW Rat; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS Rattus norvegicus.
XX
PN WO200066731-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011459.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (BIOS-) BIOSTATUM INC.
XX
PI Boutaud A;
XX
DR WPI; 2000-687538/67.
DR N-PSDB; AAC83722.
XX
PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burns, acute wounds and skin grafts.
XX
PS Claim 3; Page 117-122; 232pp; English.
XX
CC The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of Type
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotrimeric laminin, whereas

```
CC   prior art cell lines have been created that produce but do not secreted
CC   only one or two chain laminins
XX
SQ   Sequence 1694 AA;

  Query Match             100.0%;  Score 1118;  DB 3;  Length 1694;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-123;
  Matches  218;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1098 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 1157

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1158 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 1217

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1218 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 1277

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              ||||||||||||||||||||||||||||||||||||||
Db       1278 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 1315


RESULT 2
AAB48460
ID   AAB48460 standard; protein; 1725 AA.
XX
AC   AAB48460;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Rat laminin 5 polypeptide, SEQ ID NO: 10.
XX
KW   Rat; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW   cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW   periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS   Rattus norvegicus.
XX
PN   WO200066731-A2.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011459.
XX
PR   30-APR-1999;   99US-0131720P.
PR   21-AUG-1999;   99US-0149738P.
PR   24-SEP-1999;   99US-0155945P.
XX
PA   (BIOS-) BIOSTATUM INC.
XX
PI   Boutaud A;
XX
DR   WPI; 2000-687538/67.
DR   N-PSDB; AAC83721.
XX
PT   Laminin 5-expressing cells, used to accelerate wound healing associated
PT   with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT   burns, acute wounds and skin grafts.
XX
PS   Claim 3; Page 104-109; 232pp; English.
XX
CC   The present sequence is a laminin 5 chain polypeptide. Recombinant
CC   laminin 5-expressing cells are used to accelerate wound healing,
CC   especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC   surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC   intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC   improve the biocompatibility of medical devices, and to promote cell
CC   adhesion to a surface. They can be used for the ex vivo treatment of Type
CC   I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC   line produces and secretes recombinant heterotrimeric laminin, whereas
CC   prior art cell lines have been created that produce but do not secreted
CC   only one or two chain laminins
XX
SQ   Sequence 1725 AA;

  Query Match             100.0%;  Score 1118;  DB 3;  Length 1725;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-123;
  Matches  218;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1129 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 1188

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1189 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 1248

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1249 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 1308

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              ||||||||||||||||||||||||||||||||||||||
Db       1309 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 1346


RESULT 3
AAB48459
ID   AAB48459 standard; protein; 1693 AA.
XX
AC   AAB48459;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human laminin 5 polypeptide, SEQ ID NO: 8.
XX
KW   Human; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW   cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW   periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS   Homo sapiens.
XX
PN   WO200066731-A2.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011459.
XX
PR   30-APR-1999;   99US-0131720P.
PR   21-AUG-1999;   99US-0149738P.
PR   24-SEP-1999;   99US-0155945P.
XX
PA   (BIOS-) BIOSTATUM INC.
XX
PI   Boutaud A;
XX
DR   WPI; 2000-687538/67.
DR   N-PSDB; AAC83720.
XX
PT   Laminin 5-expressing cells, used to accelerate wound healing associated
PT   with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT   burns, acute wounds and skin grafts.
XX
PS   Claim 3; Page 91-97; 232pp; English.
XX
CC   The present sequence is a laminin 5 chain polypeptide. Recombinant
CC   laminin 5-expressing cells are used to accelerate wound healing,
CC   especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC   surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC   intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC   improve the biocompatibility of medical devices, and to promote cell
CC   adhesion to a surface. They can be used for the ex vivo treatment of Type
```

CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotrimeric laminin, whereas
CC prior art cell lines have been created that produce but do not secreted
CC only one or two chain laminins
XX
SQ Sequence 1693 AA;

Query Match 76.0%; Score 850; DB 3; Length 1693;
Best Local Similarity 76.6%; Pred. No. 2.6e-91;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

```
Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1098 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1157

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| ||||||:||||| ||  |||||| ||||||||:||||||
Db       1158 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1217

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1218 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1277

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
               |:| |||||||||||||| |   |||| : | :|||
Db       1278 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1315
```

RESULT 4
AAB48457
ID AAB48457 standard; protein; 1693 AA.
XX
AC AAB48457;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human laminin 5 polypeptide, SEQ ID NO: 4.
XX
KW Human; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS Homo sapiens.
XX
PN WO200066731-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011459.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (BIOS-) BIOSTATUM INC.
XX
PI Boutaud A;
XX
DR WPI; 2000-687538/67.
DR N-PSDB; AAC83718.
XX
PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burns, acute wounds and skin grafts.
XX
PS Claim 3; Page 66-71; 232pp; English.
XX
CC The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of Type
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotrimeric laminin, whereas
CC prior art cell lines have been created that produce but do not secreted
CC only one or two chain laminins
XX
SQ Sequence 1693 AA;

Query Match 76.0%; Score 850; DB 3; Length 1693;
Best Local Similarity 76.6%; Pred. No. 2.6e-91;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

```
Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1098 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1157

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| ||||||:||||| ||  |||||| ||||||||:||||||
Db       1158 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1217

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1218 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1277

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
               |:| |||||||||||||| |   |||| : | :|||
Db       1278 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1315
```

RESULT 5
AAR70148
ID AAR70148 standard; protein; 1713 AA.
XX
AC AAR70148;
XX
DT 25-MAR-2003 (revised)
DT 05-OCT-1995 (first entry)
XX
DE Deduced sequence of cDNA corresp. to the alpha-3EpA transcript.
XX
KW E170; epithelial ligand glycoprotein; epiligrin complex;
KW epithelial cell binding.
XX
OS Homo sapiens.
XX
PN WO9506660-A1.
XX
PD 09-MAR-1995.
XX
PF 02-SEP-1994; 94WO-US010261.
XX
PR 02-SEP-1993; 93US-00115918.
XX
PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
XX
PI Carter WG, Gil SG, Ryan MC;
XX
DR WPI; 1995-115398/15.
DR N-PSDB; AAQ83236.
XX
PT New nucleic acid encoding epiligrin, an epithelial ligand complex - also
PT related vectors, transformed cells, proteins and antibodies, useful
PT therapeutically and diagnostically, e.g., in cases of inflammation and to
PT induce cancer cell differentiation.
XX
PS Claim 12; Fig 15A-F; 187pp; English.
XX
CC AAQ83235 depicts the nt. sequence compiled from sequencing cDNA clones
CC corresp. to the alpha-3 EpA transcript. The invention includes nt
CC sequences in the gp. comprising the nt sequence shown in AAQ83235, the
CC cDNA clone Ep-1 (ATCC No. 75540) shown in AAQ83234, the cDNA clone 1-1
CC (ATCC No. 75539), and the cDNA clone 8-6 (ATCC No. 75538), or the nt.
CC sequences shown in AAQ83236. The entire nt region encoding E170 is

```
CC   depicted in AAQ83236, and corresp. to the SQ of alpha-3. AAQ83236
CC   consists of a composite sequence derived from several overlapping clones.
CC   A synthetic polypeptide of at least 5 AAs that corresp. to part or all of
CC   the nt. sequence shown in AAQ83236 is claimed. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 1713 AA;

  Query Match             76.0%;  Score 850;  DB 2;  Length 1713;
  Best Local Similarity   76.6%;  Pred. No. 2.6e-91;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1118 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1177

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| |||||:||||| ||  |||||| ||||||||:||||||
Db       1178 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1237

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              |||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1238 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1297

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              |:| |||||||||||||| |   |||| : | :|||
Db       1298 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 6
AAB48458
ID   AAB48458 standard; protein; 1713 AA.
XX
AC   AAB48458;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human laminin 5 polypeptide, SEQ ID NO: 6.
XX
KW   Human; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW   cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW   periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS   Homo sapiens.
XX
PN   WO200066731-A2.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011459.
XX
PR   30-APR-1999;   99US-0131720P.
PR   21-AUG-1999;   99US-0149738P.
PR   24-SEP-1999;   99US-0155945P.
XX
PA   (BIOS-) BIOSTATUM INC.
XX
PI   Boutaud A;
XX
DR   WPI; 2000-687538/67.
DR   N-PSDB; AAC83719.
XX
PT   Laminin 5-expressing cells, used to accelerate wound healing associated
PT   with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT   burns, acute wounds and skin grafts.
XX
PS   Claim 3; Page 79-84; 232pp; English.
XX
CC   The present sequence is a laminin 5 chain polypeptide. Recombinant
CC   laminin 5-expressing cells are used to accelerate wound healing,
CC   especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC   surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC   intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC   improve the biocompatibility of medical devices, and to promote cell
CC   adhesion to a surface. They can be used for the ex vivo treatment of Type
CC   I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC   line produces and secretes recombinant heterotrimeric laminin, whereas
CC   prior art cell lines have been created that produce but do not secreted
CC   only one or two chain laminins
XX
SQ   Sequence 1713 AA;

  Query Match             76.0%;  Score 850;  DB 3;  Length 1713;
  Best Local Similarity   76.6%;  Pred. No. 2.6e-91;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1118 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1177

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| |||||:||||| ||  |||||| ||||||||:||||||
Db       1178 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1237

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              |||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1238 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1297

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              |:| |||||||||||||| |   |||| : | :|||
Db       1298 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 7
ABR92102
ID   ABR92102 standard; protein; 1713 AA.
XX
AC   ABR92102;
XX
DT   10-SEP-2003  (first entry)
XX
DE   Human cervical cancer cell marker encoding cDNA SEQ ID NO:113.
XX
KW   Human; cervical cancer; cervical cancer marker; cancer therapy;
KW   detection; gene therapy; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO2002101075-A2.
XX
PD   19-DEC-2002.
XX
PF   12-JUN-2002; 2002WO-US018638.
XX
PR   13-JUN-2001; 2001US-0298155P.
PR   13-JUN-2001; 2001US-0298159P.
PR   14-NOV-2001; 2001US-0335936P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Schlegel R,  Chen Y,  Zhao X,  Monahan JE,  Kamatkar S;
PI   Gannavarapu M,  Glatt K,  Hoersch S;
XX
DR   WPI; 2003-156967/15.
DR   N-PSDB; ACF12884.
XX
PT   New isolated nucleic acid molecule useful for detecting, characterizing,
PT   preventing and treating human cervical cancers, in various prognostic and
PT   diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
XX
PS   Claim 4; Page 269-273; 386pp; English.
XX
CC   ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)
CC   given in ABR92047 to ABR92164. A higher level of expression of (I) than
CC   normal indicates the presence of cervical cancer. Also described: (1) a
CC   vector (II) containing (I); (2) a host cell (III) containing (I); and (3)
```

CC assessing (M1) whether a patient is afflicted with cervical cancer,
CC comprising comparing the level of expression of a marker in a patient's
CC sample, and the normal level of expression of the marker in a control non
CC -cervical cancer sample, where a significant increase in the level of
CC expression of the marker in the patient's sample relative to that in the
CC control sample is an indication that the patient is afflicted with
CC cervical cancer. (I) has cytostatic activity, and can be used in gene
CC therapy and in vaccines. (I) is useful in detecting, characterising,
CC preventing and treating human cervical cancers. (I) may also be used in
CC various prognostic and diagnostic assays, pharmacogenomics and in
CC monitoring clinical trials
XX
SQ Sequence 1713 AA;

Query Match 76.0%; Score 850; DB 6; Length 1713;
Best Local Similarity 76.6%; Pred. No. 2.6e-91;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

Qy 1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
Db 1118 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1177

Qy 61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
Db 1178 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1237

Qy 121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
Db 1238 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1297

Qy 181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
Db 1298 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1335

RESULT 8
ADD29904
ID ADD29904 standard; protein; 1713 AA.
XX
AC ADD29904;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human laminin alpha 3 seq id 2.
XX
KW ophthalmological; dermatological; laminin alpha 3; G3 domain;
KW cell adhesion function; cell movement effect; epithelial tissue function;
KW retinal detachment; cosmetic surgery; skin graft; human.
XX
OS Homo sapiens.
XX
PN JP2003093064-A.
XX
PD 02-APR-2003.
XX
PF 20-SEP-2001; 2001JP-00287519.
XX
PR 20-SEP-2001; 2001JP-00287519.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (KIHA-) ZH KIHARA KINEN YOKOHAMA SEIMEI KAGAKU.
XX
DR WPI; 2003-817304/77.
DR N-PSDB; ADD29903.
XX
PT Novel modified G3 domain of laminin alpha 3 chain useful for controlling
PT cell adhesion and cell movement.
XX
PS Claim 1; SEQ ID NO 2; 49pp; Japanese.
XX
CC The invention describes a modified laminin alpha3 chain comprising one or
CC more amino acid deletions, substitutions or additions at region
CC corresponding to a region of G3 domain having amino acids 1214-1324 of
CC laminin alpha3 chain having a fully defined sequence of 1713 amino acids
CC as given in the specification. (I) can control cell adhesion function and
CC cell movement effect. A composition comprising laminin is useful for
CC maintaining or treating the function of epithelial tissue and for
CC treatment or prevention of retinal detachment and in cosmetic surgery and
CC skin graft. The modified region of laminin alpha3 chain can control cell
CC adhesion function and cell movement effect. This is the amino acid
CC sequence of human laminin alpha 3.
XX
SQ Sequence 1713 AA;

Query Match 76.0%; Score 850; DB 7; Length 1713;
Best Local Similarity 76.6%; Pred. No. 2.6e-91;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

Qy 1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
Db 1118 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1177

Qy 61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
Db 1178 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1237

Qy 121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
Db 1238 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1297

Qy 181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
Db 1298 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1335

RESULT 9
ADG37225
ID ADG37225 standard; protein; 1713 AA.
XX
AC ADG37225;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human laminin-6 alpha 3 subunit.
XX
KW human; laminin-6; alpha 3; B1 subunit; B2 subunit; cell-movement;
KW cell-adhesion; dermatological; neuroprotective; muscular;
KW epithelial tissue; nervous tissue; varicella disease.
XX
OS Homo sapiens.
XX
PN JP2003212791-A.
XX
PD 30-JUL-2003.
XX
PF 17-JAN-2002; 2002JP-00009227.
XX
PR 17-JAN-2002; 2002JP-00009227.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2003-819867/77.
DR N-PSDB; ADG37224.
XX
PT Composition comprising laminin-6 for regulation of cell-movement activity
PT and/or cell-adhesion activity, useful for treating or maintaining
PT function of epithelial tissue, nervous tissue and muscles.
XX
PS Claim 2; SEQ ID NO 2; 55pp; Japanese.
XX
CC This invention describes a novel composition comprising the human laminin
CC -6 alpha 3, B1 or B2 subunits for regulation of cell-movement activity
CC and/or cell-adhesion activity. The products of the invention have
CC dermatological, neuroprotective and muscular activity. The composition of
CC the invention is useful for treating or maintaining the function of the
CC epithelial tissue, the nervous tissue and muscles and is also useful for

```
CC   treatment or prevention of varicella disease.
XX
SQ   Sequence 1713 AA;

  Query Match             76.0%;  Score 850;  DB 7;  Length 1713;
  Best Local Similarity   76.6%;  Pred. No. 2.6e-91;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1118 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1177

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| ||||||:||||| ||  |||||| ||||||||:||||||
Db       1178 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1237

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1238 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1297

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
               |:| |||||||||||||| |   |||| : | :|||
Db       1298 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 10
ABM81957
ID   ABM81957 standard; protein; 1713 AA.
XX
AC   ABM81957;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Tumour-associated antigenic target (TAT) polypeptide PRO2799, SEQ:5041.
XX
KW   Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW   tumour; diagnosis; cell proliferative disorder; breast cancer;
KW   colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW   central nervous system cancer; bladder cancer; pancreatic cancer;
KW   cervical cancer; melanoma; leukaemia; hybridisation probe;
KW   chromosome identification; chromosome mapping; gene mapping;
KW   gene therapy; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2004030615-A2.
XX
PD   15-APR-2004.
XX
PF   29-SEP-2003; 2003WO-US028547.
XX
PR   02-OCT-2002; 2002US-0414971P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Wu TD,  Zhang Z,  Zhou Y;
XX
DR   WPI; 2004-347921/32.
DR   N-PSDB; ACN40327.
XX
PT   New tumor-associated antigenic target polypeptides and nucleic acids,
PT   useful in preparing a medicament for treating or detecting a
PT   proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT   prostate cancer or tumor.
XX
PS   Claim 12; SEQ ID NO 5041; 7273pp; English.
XX
CC   The invention relates to human tumour-associated antigenic target (TAT)
CC   polypeptides, and their related nucleic acids. The TAT polypeptides are
CC   overexpressed in cancer tissues compared to normal tissues, and may thus
CC   serve as effective targets for the diagnosis and treatment of cancer in
CC   mammals. The invention also relates to nucleic acid and polypeptide
CC   sequences at least 80% identical to the TAT nucleic acids and
CC   polypeptides; expression vectors and host cells comprising a TAT nucleic
CC   acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC   molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC   TAT polypeptide; and methods and compositions for the treatment or
CC   diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC   antibodies, antagonists, binding molecules and compositions are useful
CC   for diagnosing or treating a cell proliferative disorder associated with
CC   increased TAT expression, particularly cancers such as breast cancer,
CC   colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC   cancer, pancreatic cancer, cervical cancer, cancers of the central
CC   nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC   used as hybridisation probes, in chromosome and gene mapping, in
CC   chromosome identification and in gene therapy. The present sequence
CC   represents a TAT polypeptide of the invention
XX
SQ   Sequence 1713 AA;

  Query Match             76.0%;  Score 850;  DB 8;  Length 1713;
  Best Local Similarity   76.6%;  Pred. No. 2.6e-91;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1118 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1177

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| ||||||:||||| ||  |||||| ||||||||:||||||
Db       1178 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1237

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1238 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1297

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
               |:| |||||||||||||| |   |||| : | :|||
Db       1298 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 11
ADR87606
ID   ADR87606 standard; protein; 1713 AA.
XX
AC   ADR87606;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Human Laminin alpha 3 (nicein), SEQ ID 10.
XX
KW   Cytostatic; Gene Therapy; renal cell carcinoma; Wilms tumour; human;
KW   Laminin alpha 3; nicein.
XX
OS   Homo sapiens.
XX
PN   WO2004075835-A2.
XX
PD   10-SEP-2004.
XX
PF   20-FEB-2004; 2004WO-US005042.
XX
PR   21-FEB-2003; 2003US-00372683.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Gerritsen ME,  Peale FV,  Wu TD;
XX
DR   WPI; 2004-676901/66.
DR   N-PSDB; ADR87605.
XX
PT   New anti-EDNRA antibody, useful in preparing a composition for diagnosing
PT   or inhibiting the growth of renal cell carcinoma or Wilms tumor.
XX
PS   Example 1; SEQ ID NO 10; 257pp; English.
XX
```

```
CC   The present invention relates to novel antibodies which bind to proteins
CC   which are overexpressed in renal cell carcinomas or Wilms tumour. The
CC   antibody can bind to a protein comprising CXCR4 (ADR87598), Laminin alpha
CC   4 (ADR87600), TIMP1 (ADR87602), Type IV collagen alpha 1 (ADR87604),
CC   Laminin alpha 3 (nicein) (ADR87606), Adrenomedullin (ADR87608), Type IV
CC   collagen alpha 2 (ADR87610), Thrombospondin 2 (ADR87612), Type I collagen
CC   alpha 2 (ADR87614), Type VI collagen alpha 3 (ADR87616), Latent TGFbeta
CC   binding protein 2 (LTBP2) (ADR87618), Serine or cystein protease
CC   inhibitor heat shock protein 47 (HSP47) (ADR87620), Procollagen-lysine, 2
CC   -oxoglutarate 5-dioxygenase (ADR87622), connexin 43 (ADR87624), Type IV
CC   collagen alpha 2 (ADR87626), Connexin 37 (ADR87628), Ephrin A1
CC   (ADR87630), Laminin beta 2 (ADR87632), Integrin alpha 1, hevin
CC   (ADR87635), Stanniocalcin 1 (ADR87637), Thrombospondin 4 (ADR87639), CD36
CC   polypeptide (ADR87641), Endothelin receptor A (EDNRA, ADR87643) or
CC   Endothelin receptor B (EDNRB ADR87645). The proteins of ADR87598-ADR87641
CC   and ADR87645 are all overexpressed in renal call carcinoma, and ADR87643
CC   (EDNRA) is overexpressed in Wilms tumour. The antibodies are useful in
CC   preparing a composition for diagnosing or inhibiting the growth of renal
CC   cell carcinoma or Wilms tumour. The present sequence is one such protein
CC   of the invention.
XX
SQ   Sequence 1713 AA;

  Query Match             76.0%;  Score 850;  DB 8;  Length 1713;
  Best Local Similarity   76.6%;  Pred. No. 2.6e-91;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              |||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1118 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1177

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| |||||||:||||| ||  |||||| ||||||||:|||||||
Db       1178 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1237

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::|||||||| :|||||||| ||| | ||||||| | |
Db       1238 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1297

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
               |:| |||||||||||||| |   |||| : | :|||
Db       1298 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 12
AAB48456
ID   AAB48456 standard; protein; 1724 AA.
XX
AC   AAB48456;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human laminin 5 polypeptide, SEQ ID NO: 2.
XX
KW   Human; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
KW   cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW   periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS   Homo sapiens.
XX
PN   WO200066731-A2.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011459.
XX
PR   30-APR-1999;   99US-0131720P.
PR   21-AUG-1999;   99US-0149738P.
PR   24-SEP-1999;   99US-0155945P.
XX
PA   (BIOS-) BIOSTATUM INC.
XX
PI   Boutaud A;
XX
DR   WPI; 2000-687538/67.
DR   N-PSDB; AAC83717.
XX
PT   Laminin 5-expressing cells, used to accelerate wound healing associated
PT   with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT   burns, acute wounds and skin grafts.
XX
PS   Claim 3; Page 53-59; 232pp; English.
XX
CC   The present sequence is a laminin 5 chain polypeptide. Recombinant
CC   laminin 5-expressing cells are used to accelerate wound healing,
CC   especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC   surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC   intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC   improve the biocompatibility of medical devices, and to promote cell
CC   adhesion to a surface. They can be used for the ex vivo treatment of Type
CC   I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC   line produces and secretes recombinant heterotrimeric laminin, whereas
CC   prior art cell lines have been created that produce but do not secreted
CC   only one or two chain laminins
XX
SQ   Sequence 1724 AA;

  Query Match             76.0%;  Score 850;  DB 3;  Length 1724;
  Best Local Similarity   76.6%;  Pred. No. 2.7e-91;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              |||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1129 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1188

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| |||||||:||||| ||  |||||| ||||||||:|||||||
Db       1189 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1248

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::|||||||| :|||||||| ||| | ||||||| | |
Db       1249 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1308

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
               |:| |||||||||||||| |   |||| : | :|||
Db       1309 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1346


RESULT 13
ADE08094
ID   ADE08094 standard; protein; 3332 AA.
XX
AC   ADE08094;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Novel protein (useful for identifying genetic disorders) #249.
XX
KW   novel gene; novel protein; tissue marker; molecular weight marker;
KW   chromosome marker; genetic disorder.
XX
OS   Unidentified.
XX
PN   WO2003054152-A2.
XX
PD   03-JUL-2003.
XX
PF   10-DEC-2002; 2002WO-US039555.
XX
PR   10-DEC-2001; 2001US-0339739P.
PR   11-DEC-2001; 2001US-0339453P.
PR   14-MAR-2002; 2002US-0365091P.
PR   14-MAR-2002; 2002US-0365384P.
PR   12-APR-2002; 2002US-0372381P.
PR   12-APR-2002; 2002US-0372615P.
PR   22-APR-2002; 2002US-00128558.
```

PR 24-APR-2002; 2002US-0376045P.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
DR WPI; 2003-569235/53.
DR N-PSDB; ADE07183.
XX
PT New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.
XX
PS Claim 20; SEQ ID NO 1160; 1177pp; English.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present amino acid sequence represents a protein
CC of the invention.
XX
SQ Sequence 3332 AA;

Query Match 76.0%; Score 850; DB 7; Length 3332;
Best Local Similarity 76.6%; Pred. No. 7.4e-91;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

```
Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       2737 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 2796

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| ||||||:||||| ||  |||||| ||||||||:||||||
Db       2797 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 2856

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       2857 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 2916

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
               |:| |||||||||||||||| |   |||| : | :|||
Db       2917 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 2954
```

RESULT 14
AAG75103
ID AAG75103 standard; protein; 469 AA.
XX
AC AAG75103;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:5867.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 18.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US026524.
XX
PR 29-SEP-1999; 99US-0157137P.
PR 03-NOV-1999; 99US-0163280P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
DR N-PSDB; AAH34508.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS Claim 11; Page 7385-7387; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patients own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
XX
SQ Sequence 469 AA;

Query Match 60.8%; Score 680; DB 4; Length 469;
Best Local Similarity 72.2%; Pred. No. 8e-72;
Matches 135; Conservative 17; Mismatches 35; Indels 0; Gaps 0;

```
Qy         32 TASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELS 91
              :|||||| |:|||:| :| ||  | |||||||||||| ||:||| |  | |||||:||||
Db          1 SASFSRGXQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQTWTRXLQVTLEDGYIELS 60

Qy         92 TRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQQSLRLG 151
              | ||  |||||| ||||||||:|||||| ||||||||||:|| ::||   |:::||||||
Db         61 TSDSXGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLRNSKRLKHISSSRQSLRLG 120

Qy        152 GGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNKGR 211
              | :|||||||| ||| | ||||||| | | |:| |||||||||||||| |   |||| :
Db        121 GSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLNKPPFLMLLKGSTRFNKTK 180

Qy        212 IFNVNQL 218
               | :|||
Db        181 TFRINQL 187
```

RESULT 15
AAB48447
ID AAB48447 standard; protein; 1792 AA.
XX
AC AAB48447;
XX
DT 02-MAR-2001 (first entry)
XX
DE Mouse laminin 8 polypeptide, SEQ ID NO: 12.
XX
KW Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;
KW antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
KW vascular tissue injury; neural injury; angiogenesis regulation.
XX
OS Mus musculus.
XX
PN WO200066732-A2.
XX
PD 09-NOV-2000.

XX
PF 28-APR-2000; 2000WO-US011543.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
PI Kortesmaa J, Tryggvason K;
XX
DR WPI; 2000-687539/67.
DR N-PSDB; AAC83708.
XX
PT Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 136-142; 245pp; English.
XX
CC The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament,
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
CC migration
XX
SQ Sequence 1792 AA;

Query Match 18.2%; Score 204; DB 3; Length 1792;
Best Local Similarity 29.1%; Pred. No. 6.6e-14;
Matches 64; Conservative 35; Mismatches 99; Indels 22; Gaps 8;

```
Qy          5 KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD-VPSTDRFQLSFGFQTF 63
              ||    ::   :|:||   | ||  : | | |:  ||    ::  :   | |:  | |:|
Db       1180 KKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIASIQKISFFDGFEGGFNFRTL 1237

Qy         64 QPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHH-VSVISDTSG 122
              ||:| |  : : :    ::|::| : :  :   | :  :   | ||| |  |: ||||
Db       1238 QPNGLLFYYTSGSDVFSISLDNGTVVMDVK--GIKVMSTDKQYHDGLPHFVVTSISDTR- 1294

Qy        123 LRLLIDDQVLRRNQRLPSFSNAQQS------LRLGG-------GHFEGCISNVLVQRFSQ 169
               |::|   ||     |:   |:|:         ||        :| |||||    |  :
Db       1295 YELVVDKSRLRGKN--PTKGKAEQTQTTEKKFYFGGSPISPQYANFTGCISNAYFTRLDR 1352

Qy        170 SPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 209
               || |   | |   ||  | :   |  :| |  |  :|
Db       1353 DVEVEDFQRYSEKVHTSLYECPIESSPLFLLHKKGKNSSK 1392
```

Search completed: February 22, 2005, 08:18:48
Job time : 41.1892 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:19:00 ; Search time 29.2165 Seconds
(without alignments)
2441.722 Million cell updates/sec

Title: US-10-817-423-6
Perfect score: 1118
Sequence: 1 MKNLKKTSGVVRLNDTVGVT.....MLFKSPKRFNKGRIFNVNQL 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1118	100.0	1694	15	US-10-603-725-12	Sequence 12, Appl
2	1118	100.0	1725	15	US-10-603-725-10	Sequence 10, Appl
3	850	76.0	1693	15	US-10-603-725-4	Sequence 4, Appli
4	850	76.0	1693	15	US-10-603-725-8	Sequence 8, Appli
5	850	76.0	1713	14	US-10-171-311-113	Sequence 113, App
6	850	76.0	1713	15	US-10-372-683-10	Sequence 10, Appl
7	850	76.0	1713	15	US-10-603-725-6	Sequence 6, Appli
8	850	76.0	1724	15	US-10-603-725-2	Sequence 2, Appli
9	680	60.8	469	14	US-10-106-698-5877	Sequence 5877, Ap
10	187	16.7	1581	16	US-10-408-765A-154	Sequence 154, App
11	187	16.7	1816	14	US-10-299-058-2	Sequence 2, Appli
12	187	16.7	1816	14	US-10-299-058-4	Sequence 4, Appli
13	187	16.7	1816	15	US-10-372-683-4	Sequence 4, Appli
14	187	16.7	1823	15	US-10-363-616-457	Sequence 457, App
15	186	16.6	3635	9	US-09-845-583-2	Sequence 2, Appli
16	186	16.6	3635	14	US-10-037-182-4	Sequence 4, Appli
17	186	16.6	3635	15	US-10-037-417-47	Sequence 47, Appl
18	176	15.7	3597	15	US-10-037-417-6	Sequence 6, Appli
19	176	15.7	3600	15	US-10-037-417-2	Sequence 2, Appli
20	176	15.7	3690	15	US-10-112-944-347	Sequence 347, App
21	175	15.7	49	9	US-09-925-299-1149	Sequence 1149, Ap
22	175	15.7	49	10	US-09-925-299-1149	Sequence 1149, Ap
23	174	15.6	463	15	US-10-264-049-3039	Sequence 3039, Ap
24	174	15.6	908	15	US-10-037-417-4	Sequence 4, Appli
25	174	15.6	953	9	US-09-845-583-4	Sequence 4, Appli
26	174	15.6	953	15	US-10-037-417-50	Sequence 50, Appl
27	174	15.6	1634	15	US-10-037-417-49	Sequence 49, Appl
28	174	15.6	1640	15	US-10-037-417-8	Sequence 8, Appli
29	174	15.6	1677	15	US-10-112-944-801	Sequence 801, App
30	174	15.6	3695	14	US-10-037-182-2	Sequence 2, Appli
31	174	15.6	3695	15	US-10-312-352-22	Sequence 22, Appl
32	174	15.6	3696	15	US-10-312-088-31	Sequence 31, Appl
33	174	15.6	3705	15	US-10-312-088-30	Sequence 30, Appl
34	173.5	15.5	3712	13	US-10-108-605-103	Sequence 103, App
35	173.5	15.5	3712	15	US-10-037-417-48	Sequence 48, Appl
36	173.5	15.5	3712	15	US-10-037-417-51	Sequence 51, Appl
37	151.5	13.6	365	9	US-09-925-299-1007	Sequence 1007, Ap
38	151.5	13.6	365	10	US-09-925-299-1007	Sequence 1007, Ap
39	134.5	12.0	3070	10	US-09-961-403-7	Sequence 7, Appli
40	128.5	11.5	2923	9	US-09-788-711A-4	Sequence 4, Appli
41	128.5	11.5	2923	10	US-09-916-849A-3	Sequence 3, Appli
42	128.5	11.5	2923	14	US-10-225-567A-524	Sequence 524, App
43	128.5	11.5	2923	14	US-10-174-677-29	Sequence 29, Appl
44	128.5	11.5	2923	15	US-10-120-801-53	Sequence 53, Appl
45	128.5	11.5	2923	15	US-10-292-798-932	Sequence 932, App

ALIGNMENTS

RESULT 1
US-10-603-725-12
; Sequence 12, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boutand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1694
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-603-725-12

Query Match 100.0%; Score 1118; DB 15; Length 1694;
Best Local Similarity 100.0%; Pred. No. 7e-109;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1098 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 1157

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1158 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 1217

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1218 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 1277

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              ||||||||||||||||||||||||||||||||||||||
```

```
Db       1278 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 1315


RESULT 2
US-10-603-725-10
; Sequence 10, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
;  APPLICANT: Boutand, Ariel
;  TITLE OF INVENTION: Recombinant Laminin 5
;  FILE REFERENCE: 99-274-C
;  CURRENT APPLICATION NUMBER: US/10/603,725
;  CURRENT FILING DATE:  2003-06-25
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 1725
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-603-725-10

  Query Match            100.0%;  Score 1118;  DB 15;  Length 1725;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-109;
  Matches  218;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1129 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 1188

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1189 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 1248

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1249 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 1308

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              ||||||||||||||||||||||||||||||||||||||
Db       1309 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 1346


RESULT 3
US-10-603-725-4
; Sequence 4, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
;  APPLICANT: Boutand, Ariel
;  TITLE OF INVENTION: Recombinant Laminin 5
;  FILE REFERENCE: 99-274-C
;  CURRENT APPLICATION NUMBER: US/10/603,725
;  CURRENT FILING DATE:  2003-06-25
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1693
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-603-725-4

  Query Match             76.0%;  Score 850;  DB 15;  Length 1693;
  Best Local Similarity   76.6%;  Pred. No. 2e-80;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1098 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1157

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| ||||||:||||| ||  |||||| ||||||||:||||||
Db       1158 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1217

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1218 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1277

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              |:| |||||||||||||| |   |||| : | :|||
Db       1278 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1315


RESULT 4
US-10-603-725-8
; Sequence 8, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
;  APPLICANT: Boutand, Ariel
;  TITLE OF INVENTION: Recombinant Laminin 5
;  FILE REFERENCE: 99-274-C
;  CURRENT APPLICATION NUMBER: US/10/603,725
;  CURRENT FILING DATE:  2003-06-25
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 1693
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-603-725-8

  Query Match             76.0%;  Score 850;  DB 15;  Length 1693;
  Best Local Similarity   76.6%;  Pred. No. 2e-80;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1098 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1157

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| ||||||:||||| ||  |||||| ||||||||:||||||
Db       1158 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1217

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1218 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1277

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              |:| |||||||||||||| |   |||| : | :|||
Db       1278 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1315


RESULT 5
US-10-171-311-113
; Sequence 113, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
;  APPLICANT: Schlegel, Robert
;  APPLICANT:  Chen, Yan
;  APPLICANT:  Zhao, Xumei
;  APPLICANT:  Monahan, John
;  APPLICANT:  Kamatkar, Shubhangi
;  APPLICANT:  Glatt, Karen
;  APPLICANT:  Gannavarapu, Manjula
;  APPLICANT:  Hoersh, Sebastian
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
;  TITLE OF INVENTION:  OF CERVICAL CANCER
;  FILE REFERENCE: MRI-035
;  CURRENT APPLICATION NUMBER: US/10/171,311
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: US 60/298,159
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,155
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/335,936
;  PRIOR FILING DATE: 2001-11-14
;  NUMBER OF SEQ ID NOS: 238
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 113
;   LENGTH: 1713
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-171-311-113

  Query Match             76.0%;  Score 850;  DB 14;  Length 1713;
  Best Local Similarity   76.6%;  Pred. No. 2e-80;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1118 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1177

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| |||||||:||||| ||  |||||| ||||||||:||||||
Db       1178 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1237

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1238 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1297

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
               |:| |||||||||||||| |   |||| : | :|||
Db       1298 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 6
US-10-372-683-10
; Sequence 10, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
;  APPLICANT: GERRITSEN, MARY E.
;  APPLICANT:  PEALE JR., FRANKLIN V.
;  APPLICANT:  WU, THOMAS D.
;  TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
;  FILE REFERENCE: P1928R1P1
;  CURRENT APPLICATION NUMBER: US/10/372,683
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US 10/271,690
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/344,534
;  PRIOR FILING DATE: 2001-10-18
;  NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 10
;   LENGTH: 1713
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-372-683-10

  Query Match             76.0%;  Score 850;  DB 15;  Length 1713;
  Best Local Similarity   76.6%;  Pred. No. 2e-80;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1118 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1177

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| |||||||:||||| ||  |||||| ||||||||:||||||
Db       1178 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1237

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1238 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1297

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
               |:| |||||||||||||| |   |||| : | :|||
Db       1298 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 7
US-10-603-725-6
; Sequence 6, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
;  APPLICANT: Boutand, Ariel
;  TITLE OF INVENTION: Recombinant Laminin 5
;  FILE REFERENCE: 99-274-C
;  CURRENT APPLICATION NUMBER: US/10/603,725
;  CURRENT FILING DATE:  2003-06-25
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 1713
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-603-725-6

  Query Match             76.0%;  Score 850;  DB 15;  Length 1713;
  Best Local Similarity   76.6%;  Pred. No. 2e-80;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1118 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1177

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| |||||||:||||| ||  |||||| ||||||||:||||||
Db       1178 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1237

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1238 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1297

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
               |:| |||||||||||||| |   |||| : | :|||
Db       1298 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 8
US-10-603-725-2
; Sequence 2, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
;  APPLICANT: Boutand, Ariel
;  TITLE OF INVENTION: Recombinant Laminin 5
;  FILE REFERENCE: 99-274-C
;  CURRENT APPLICATION NUMBER: US/10/603,725
;  CURRENT FILING DATE:  2003-06-25
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1724
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-603-725-2

  Query Match             76.0%;  Score 850;  DB 15;  Length 1724;
  Best Local Similarity   76.6%;  Pred. No. 2e-80;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1129 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1188

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| |||||||:||||| ||  |||||| ||||||||:||||||
Db       1189 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1248

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1249 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1308

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
```

```
              |:| |||||||||||||||| |   |||| : | :|||
Db       1309 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1346


RESULT 9
US-10-106-698-5877
; Sequence 5877, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
;  FILE REFERENCE: PA005P1
;  CURRENT APPLICATION NUMBER: US/10/106,698
;  CURRENT FILING DATE:  2002-03-27
;  PRIOR APPLICATION NUMBER: PCT/US00/26524
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US 60/157,137
;  PRIOR FILING DATE: 1999-09-29
;  PRIOR APPLICATION NUMBER: US 60/163,280
;  PRIOR FILING DATE: 1999-11-03
;  NUMBER OF SEQ ID NOS: 8564
;  SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 5877
;   LENGTH: 469
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (8)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (47)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (65)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (436)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5877

  Query Match             60.8%;  Score 680;  DB 14;  Length 469;
  Best Local Similarity   72.2%;  Pred. No. 3.6e-63;
  Matches  135;  Conservative   17;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          32 TASFSRGGQMSFTNLDVPSTDRFQLSFGFQTFQPSGTLLNHQTRTSSLLVTLEDGHIELS 91
               :|||||| |:|||:| :| ||  | |||||||||||| ||:||| |  | |||||:||||
Db           1 SASFSRGXQLSFTDLGLPPTDHLQASFGFQTFQPSGILLDHQTWTRXLQVTLEDGYIELS 60

Qy          92 TRDSNIPIFKSPGTYMDGLLHHVSVISDTSGLRLLIDDQVLRRNQRLPSFSNAQQSLRLG 151
               | ||  |||||| ||||||||:|||||| ||||||||||:|| ::||   |:::|||||
Db          61 TSDSXGPIFKSPQTYMDGLLHYVSVISDNSGLRLLIDDQLLRNSKRLKHISSSRQSLRLG 120

Qy         152 GGHFEGCISNVLVQRFSQSPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNKGR 211
               | :|||||||| ||| | |||||| | | |:| |||||||||||||| |   |||| :
Db         121 GSNFEGCISNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLNKPPFLMLLKGSTRFNKTK 180

Qy         212 IFNVNQL 218
               | :|||
Db         181 TFRINQL 187


RESULT 10
US-10-408-765A-154
; Sequence 154, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
;  APPLICANT: Ghosh, Soumitra S.
;  APPLICANT:  Fahy, Eoin D.
;  APPLICANT:  Zhang, Bing
;  APPLICANT:  Gibson, Bradford W.
;  APPLICANT:  Taylor, Steven W.
;  APPLICANT:  Glenn, Gary M.
;  APPLICANT:  Warnock, Dale E.
;  TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
;  TITLE OF INVENTION:  IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
;  FILE REFERENCE: 660088.465
;  CURRENT APPLICATION NUMBER: US/10/408,765A
;  CURRENT FILING DATE:  2003-04-04
;  NUMBER OF SEQ ID NOS: 3077
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 154
;   LENGTH: 1581
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-765A-154

  Query Match             16.7%;  Score 187;  DB 16;  Length 1581;
  Best Local Similarity   28.3%;  Pred. No. 4.3e-10;
  Matches   62;  Conservative   34;  Mismatches  103;  Indels   20;  Gaps    8;

Qy           5 KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD-VPSTDRFQLSFGFQTF 63
               ||   ::   :|:||   | ||  : | | |:  ||    ::  :   | |:  | |:|
Db         967 KKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIASIQKISFFDGFEGGFNFRTL 1024

Qy          64 QPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGL 123
               ||:| |  : : :    ::|::| : :  :   | :       | ||| |   ||| |
Db        1025 QPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQSVDKQYNDGLSHF--VISSVSPT 1080

Qy         124 R--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-------GHFEGCISNVLVQRFSQS 170
               |  |::|  :|  :|          | | :    ||        :| |||||    |  :
Db        1081 RYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSPISAQYANFTGCISNAYFTRVDRD 1140

Qy         171 PEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 209
               || |    : |   ||  | :   |  :| |  |  :|
Db        1141 VEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNLSK 1179


RESULT 11
US-10-299-058-2
; Sequence 2, Application US/10299058
; Publication No. US20030103975A1
; GENERAL INFORMATION:
;  APPLICANT: JONES, JONATHAN C.R.
;  APPLICANT:  GONZALES, MEREDITH
;  TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHELIALIZATION
;  FILE REFERENCE: 1720-1-002 CIP
;  CURRENT APPLICATION NUMBER: US/10/299,058
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 09/706,235
;  PRIOR FILING DATE: 2000-11-03
;  PRIOR APPLICATION NUMBER: 60/163,199
;  PRIOR FILING DATE: 1999-11-03
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1816
;   TYPE: PRT
;   ORGANISM: Homo sapien
;   FEATURE:
;   OTHER INFORMATION: X in position 1112 = Arg/Pro
US-10-299-058-2

  Query Match             16.7%;  Score 187;  DB 14;  Length 1816;
  Best Local Similarity   28.3%;  Pred. No. 5.3e-10;
  Matches   62;  Conservative   34;  Mismatches  103;  Indels   20;  Gaps    8;

Qy           5 KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD-VPSTDRFQLSFGFQTF 63
               ||   ::   :|:||   | ||  : | | |:  ||    ::  :   | |:  | |:|
Db        1202 KKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIASIQKISFFDGFEGGFNFRTL 1259

Qy          64 QPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGL 123
               ||:| |  : : :    ::|::| : :  :   | :       | ||| |   ||| |
Db        1260 QPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQSVDKQYNDGLSHF--VISSVSPT 1315

Qy         124 R--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-------GHFEGCISNVLVQRFSQS 170
```

```
                |  |::|  :|  :|          | | :    ||        :| |||||    |  :
Db       1316 RYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSPISAQYANFTGCISNAYFTRVDRD 1375

Qy        171 PEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 209
              || |    : |   ||  | :  | :| |  |  :|
Db       1376 VEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNLSK 1414
```

RESULT 12
US-10-299-058-4
; Sequence 4, Application US/10299058
; Publication No. US20030103975A1
; GENERAL INFORMATION:
; APPLICANT: JONES, JONATHAN C.R.
; APPLICANT: GONZALES, MEREDITH
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHELIALIZATION
; FILE REFERENCE: 1720-1-002 CIP
; CURRENT APPLICATION NUMBER: US/10/299,058
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/706,235
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/163,199
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1816
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; OTHER INFORMATION: X in position 1112 = R/P
US-10-299-058-4

Query Match 16.7%; Score 187; DB 14; Length 1816;
Best Local Similarity 28.3%; Pred. No. 5.3e-10;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

```
Qy          5 KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD-VPSTDRFQLSFGFQTF 63
              ||   ::   :|:||   | ||  : | | |:  ||    ::  :   | |:  | |:|
Db       1202 KKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIASIQKISFFDGFEGGFNFRTL 1259

Qy         64 QPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGL 123
              ||:| |  : : :    ::|::| : :  :   | :      | ||| |   |||  |
Db       1260 QPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQSVDKQYNDGLSHF--VISSVSPT 1315

Qy        124 R--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-------GHFEGCISNVLVQRFSQS 170
              |  |::|  :|  :|          | | :    ||        :| |||||    |  :
Db       1316 RYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSPISAQYANFTGCISNAYFTRVDRD 1375

Qy        171 PEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 209
              || |    : |   ||  | :  | :| |  |  :|
Db       1376 VEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNLSK 1414
```

RESULT 13
US-10-372-683-4
; Sequence 4, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: PEALE JR., FRANKLIN V.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 4
; LENGTH: 1816
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-372-683-4

Query Match 16.7%; Score 187; DB 15; Length 1816;
Best Local Similarity 28.3%; Pred. No. 5.3e-10;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

```
Qy          5 KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD-VPSTDRFQLSFGFQTF 63
              ||   ::   :|:||   | ||  : | | |:  ||    ::  :   | |:  | |:|
Db       1202 KKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIASIQKISFFDGFEGGFNFRTL 1259

Qy         64 QPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGL 123
              ||:| |  : : :    ::|::| : :  :   | :      | ||| |   |||  |
Db       1260 QPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQSVDKQYNDGLSHF--VISSVSPT 1315

Qy        124 R--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-------GHFEGCISNVLVQRFSQS 170
              |  |::|  :|  :|          | | :    ||        :| |||||    |  :
Db       1316 RYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSPISAQYANFTGCISNAYFTRVDRD 1375

Qy        171 PEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 209
              || |    : |   ||  | :  | :| |  |  :|
Db       1376 VEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNLSK 1414
```

RESULT 14
US-10-363-616-457
; Sequence 457, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 457
; LENGTH: 1823
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-457

Query Match 16.7%; Score 187; DB 15; Length 1823;
Best Local Similarity 28.3%; Pred. No. 5.3e-10;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

```
Qy          5 KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD-VPSTDRFQLSFGFQTF 63
              ||   ::   :|:||   | ||  : | | |:  ||    ::  :   | |:  | |:|
Db       1209 KKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIASIQKISFFDGFEGGFNFRTL 1266

Qy         64 QPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGL 123
              ||:| |  : : :    ::|::| : :  :   | :      | ||| |   |||  |
Db       1267 QPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQSVDKQYNDGLSHF--VISSVSPT 1322

Qy        124 R--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-------GHFEGCISNVLVQRFSQS 170
              |  |::|  :|  :|          | | :    ||        :| |||||    |  :
Db       1323 RYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSPISAQYANFTGCISNAYFTRVDRD 1382

Qy        171 PEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 209
              || |    : |   ||  | :  | :| |  |  :|
Db       1383 VEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNLSK 1421
```

RESULT 15
US-09-845-583-2
; Sequence 2, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champliaud, Marie-France

```
;  APPLICANT:  Hunter, Dale
;  TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
;  FILE REFERENCE: 10287-056001
;  CURRENT APPLICATION NUMBER: US/09/845,583
;  CURRENT FILING DATE:  2001-04-30
;  PRIOR APPLICATION NUMBER: US 60/200,863
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 3635
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-845-583-2

  Query Match             16.6%;  Score 186;  DB 9;  Length 3635;
  Best Local Similarity   29.2%;  Pred. No. 1.8e-09;
  Matches   59;  Conservative   34;  Mismatches   91;  Indels   18;  Gaps    6;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDV-PSTDRFQLSFG 59
              :| | |   : ||| | |::  |: |  : || :|   | :     || | |:     ||
Db       3015 IKALGKYVDLKRLN-TTGISFGCTADLLVGRTMTFHGHGFLPLALPDVAPITEVVYSGFG 3073

Qy         60 FQTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISD 119
              |:  | :  |    :       |:| :||: |   :  :   ::   : ||  |:|:  |:
Db       3074 FRGTQDNNLLYYRTSPDGPYQVSLREGHVTLRFMNQEV---ETQRVFADGAPHYVAFYSN 3130

Qy        120 TSGLRLLIDD--QVLRRNQRLPSFSNAQ----QSLRLGG-------GHFEGCISNVLVQR 166
              :|: | :||  |::: ::|       |       | |||         :| |||||| |||
Db       3131 VTGVWLYVDDQLQLVKSHERTTPMLQLQPEEPSRLLLGGLPVSGTFHNFSGCISNVFVQR 3190

Qy        167 FSQSPEVLDLASKSTKKDASLG 188
                | ||       : |:|
Db       3191 LRGPQRVFDLHQNMGSVNVSVG 3212


Search completed: February 22, 2005, 08:44:42
Job time : 29.2165 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:13:40 ; Search time 10.1795 Seconds
(without alignments)
1598.653 Million cell updates/sec

Title: US-10-817-423-6
Perfect score: 1118
Sequence: 1 MKNLKKTSGVVRLNDTVGVT.....MLFKSPKRFNKGRIFNVNQL 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1118	100.0	1694	4	US-09-560-385A-12	Sequence 12, Appl
2	1118	100.0	1725	4	US-09-560-385A-10	Sequence 10, Appl
3	850	76.0	1693	4	US-09-560-385A-4	Sequence 4, Appli
4	850	76.0	1693	4	US-09-560-385A-8	Sequence 8, Appli
5	850	76.0	1713	3	US-08-600-982-24	Sequence 24, Appl
6	850	76.0	1713	4	US-09-560-385A-6	Sequence 6, Appli
7	850	76.0	1713	4	US-09-538-092-1359	Sequence 1359, Ap
8	850	76.0	1713	5	PCT-US94-10261A-24	Sequence 24, Appl
9	850	76.0	1724	4	US-09-560-385A-2	Sequence 2, Appli
10	204	18.2	1792	4	US-09-561-818A-12	Sequence 12, Appl
11	204	18.2	1816	4	US-09-561-818A-10	Sequence 10, Appl
12	187	16.7	1792	4	US-09-561-818A-4	Sequence 4, Appli
13	187	16.7	1800	4	US-09-561-818A-8	Sequence 8, Appli
14	187	16.7	1816	4	US-09-561-818A-2	Sequence 2, Appli
15	187	16.7	1824	4	US-09-561-818A-6	Sequence 6, Appli
16	186	16.6	3635	4	US-09-845-583A-2	Sequence 2, Appli
17	174	15.6	953	4	US-09-845-583A-4	Sequence 4, Appli
18	174	15.6	3647	4	US-09-949-016-10932	Sequence 10932, A
19	144.5	12.9	3084	4	US-09-562-702A-12	Sequence 12, Appl
20	144.5	12.9	3106	4	US-09-562-702A-10	Sequence 10, Appl
21	137.5	12.3	1130	6	5444158-2	Patent No. 5444158
22	137.5	12.3	1130	6	5444158-2	Patent No. 5444158
23	134.5	12.0	1130	2	US-08-460-309-2	Sequence 2, Appli
24	134.5	12.0	1130	2	US-08-125-077-2	Sequence 2, Appli
25	134.5	12.0	3070	4	US-09-961-403-7	Sequence 7, Appli
26	134.5	12.0	3088	4	US-09-562-702A-8	Sequence 8, Appli
27	134.5	12.0	3089	4	US-09-562-702A-4	Sequence 4, Appli
28	134.5	12.0	3110	4	US-09-562-702A-2	Sequence 2, Appli
29	134.5	12.0	3110	4	US-09-562-702A-6	Sequence 6, Appli
30	134.5	12.0	3110	4	US-09-561-709B-7	Sequence 7, Appli
31	134.5	12.0	3110	4	US-09-917-254-86	Sequence 86, Appl
32	134.5	12.0	3110	4	US-09-949-016-5937	Sequence 5937, Ap
33	134.5	12.0	3111	2	US-08-460-309-4	Sequence 4, Appli
34	134.5	12.0	3111	2	US-08-125-077-4	Sequence 4, Appli
35	101.5	9.1	3075	2	US-08-460-309-5	Sequence 5, Appli
36	101.5	9.1	3075	2	US-08-125-077-5	Sequence 5, Appli
37	98.5	8.8	21	1	US-08-445-135-7	Sequence 7, Appli
38	94.5	8.5	675	6	5258288-1	Patent No. 5258288
39	94.5	8.5	675	6	5258288-1	Patent No. 5258288
40	91	8.1	212	4	US-09-270-767-43408	Sequence 43408, A
41	89.5	8.0	1381	4	US-08-826-134-4	Sequence 4, Appli
42	84.5	7.6	1384	4	US-09-949-016-7814	Sequence 7814, Ap
43	84	7.5	814	4	US-09-486-072-1	Sequence 1, Appli
44	83.5	7.5	1331	4	US-09-949-016-6861	Sequence 6861, Ap
45	82	7.3	271	2	US-08-956-012-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-560-385A-12
; Sequence 12, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Boutand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1694
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-560-385A-12

Query Match 100.0%; Score 1118; DB 4; Length 1694;
Best Local Similarity 100.0%; Pred. No. 5e-124;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1098 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 1157

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1158 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 1217

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1218 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 1277

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              |||||||||||||||||||||||||||||||||||||
Db       1278 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 1315
```

RESULT 2
US-09-560-385A-10
; Sequence 10, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Boutand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36

```
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 1725
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-560-385A-10

  Query Match             100.0%;  Score 1118;  DB 4;  Length 1725;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-124;
  Matches  218;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1129 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 1188

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1189 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 1248

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1249 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 1308

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              |||||||||||||||||||||||||||||||||||||
Db       1309 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 1346


RESULT 3
US-09-560-385A-4
; Sequence 4, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
;  APPLICANT:  Boutand, Ariel
;  TITLE OF INVENTION:  Recombinant Laminin 5
;  FILE REFERENCE:  99-274-C
;  CURRENT APPLICATION NUMBER: US/09/560,385A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1693
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-560-385A-4

  Query Match             76.0%;  Score 850;  DB 4;  Length 1693;
  Best Local Similarity   76.6%;  Pred. No. 6.5e-92;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||||:||||||:|||:| :| ||  | ||||
Db       1098 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1157

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| |||||:||||| ||  |||||| ||||||||:||||||
Db       1158 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1217

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1218 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1277

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              |:| |||||||||||||| |   |||| : | :|||
Db       1278 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1315


RESULT 4
US-09-560-385A-8
; Sequence 8, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
;  APPLICANT:  Boutand, Ariel
;  TITLE OF INVENTION:  Recombinant Laminin 5
;  FILE REFERENCE:  99-274-C
;  CURRENT APPLICATION NUMBER: US/09/560,385A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 1693
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-560-385A-8

  Query Match             76.0%;  Score 850;  DB 4;  Length 1693;
  Best Local Similarity   76.6%;  Pred. No. 6.5e-92;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||:|||:| :| ||  | ||||
Db       1098 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1157

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| |||||:||||| ||  |||||| ||||||||:||||||
Db       1158 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1217

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1218 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1277

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              |:| |||||||||||||| |   |||| : | :|||
Db       1278 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1315


RESULT 5
US-08-600-982-24
; Sequence 24, Application US/08600982
; Patent No. 6120991
;  GENERAL INFORMATION:
;    APPLICANT:  Carter, William G.
;    APPLICANT:  Gil, Susanna A.
;    APPLICANT:  Ryan, Maureen C.
;    TITLE OF INVENTION:  Epiligrin, an Epithelial Ligand for
;    TITLE OF INVENTION:  Integrins
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen, O'Connor, Johnson, and Kindness
;      STREET:  1420 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101-8100
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/600,982
;      FILING DATE:  02-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Shelton, Dennis K.
;      REGISTRATION NUMBER:  26,997
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 682-8100
;      TELEFAX:  (206) 224-0779
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1713 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;      DESCRIPTION:  E170 protein as translated from sequence
```

```
;      DESCRIPTION:  of FIGURES 15A-15F, and as shown also in FIGURES
;      DESCRIPTION:  19A-19R
US-08-600-982-24

  Query Match             76.0%;  Score 850;  DB 3;  Length 1713;
  Best Local Similarity   76.6%;  Pred. No. 6.6e-92;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1118 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1177

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| ||||||:||||| ||  |||||| ||||||||:||||||
Db       1178 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1237

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1238 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1297

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              |:| |||||||||||||||  |   |||| : | :|||
Db       1298 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 6
US-09-560-385A-6
; Sequence 6, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
;  APPLICANT:  Boutand, Ariel
;  TITLE OF INVENTION:  Recombinant Laminin 5
;  FILE REFERENCE:  99-274-C
;  CURRENT APPLICATION NUMBER: US/09/560,385A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 1713
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-560-385A-6

  Query Match             76.0%;  Score 850;  DB 4;  Length 1713;
  Best Local Similarity   76.6%;  Pred. No. 6.6e-92;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1118 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1177

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| ||||||:||||| ||  |||||| ||||||||:||||||
Db       1178 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1237

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1238 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1297

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              |:| |||||||||||||||  |   |||| : | :|||
Db       1298 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 7
US-09-538-092-1359
; Sequence 1359, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1359
;   LENGTH: 1713
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number Q16787
US-09-538-092-1359

  Query Match             76.0%;  Score 850;  DB 4;  Length 1713;
  Best Local Similarity   76.6%;  Pred. No. 6.6e-92;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1118 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1177

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| ||||||:||||| ||  |||||| ||||||||:||||||
Db       1178 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1237

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              ||||||||||:|| ::||   |:::||||||| :|||||||| ||| | ||||||| | |
Db       1238 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1297

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              |:| |||||||||||||||  |   |||| : | :|||
Db       1298 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 8
PCT-US94-10261A-24
; Sequence 24, Application PC/TUS9410261A
;  GENERAL INFORMATION:
;    APPLICANT:  Carter, William G.
;    APPLICANT:  Gil, Susanna A.
;    APPLICANT:  Ryan, Maureen C.
;    TITLE OF INVENTION:  Epiligrin, an Epithelial Ligand for
;    TITLE OF INVENTION:  Integrins
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen, O'Connor, Johnson, and Kindness
;      STREET:  1420 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101-8100
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10261A
;      FILING DATE:  02-SEP-1994
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Shelton, Dennis K.
;      REGISTRATION NUMBER:  26,997
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 682-8100
;      TELEFAX:  (206) 224-0779
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
```

```
;      LENGTH:  1713 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;      DESCRIPTION:  E170 protein as translated from sequence of
;      DESCRIPTION:  FIGURES 15A-15F, and as shown also in FIGURES 19A-19R
PCT-US94-10261A-24

  Query Match             76.0%;  Score 850;  DB 5;  Length 1713;
  Best Local Similarity   76.6%;  Pred. No. 6.6e-92;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1118 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1177

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| |||||||:||||| ||  |||||| ||||||||:||||||
Db       1178 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1237

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              |||||||||||:|| ::||    |:::||||||| :|||||||| ||| | ||||||| | |
Db       1238 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1297

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              |:| |||||||||||||| |   |||| : | :|||
Db       1298 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1335


RESULT 9
US-09-560-385A-2
; Sequence 2, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
;  APPLICANT:  Boutand, Ariel
;  TITLE OF INVENTION:  Recombinant Laminin 5
;  FILE REFERENCE:  99-274-C
;  CURRENT APPLICATION NUMBER: US/09/560,385A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1724
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-560-385A-2

  Query Match             76.0%;  Score 850;  DB 4;  Length 1724;
  Best Local Similarity   76.6%;  Pred. No. 6.7e-92;
  Matches  167;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLDVPSTDRFQLSFGF 60
              ||||||||||||||||||||||||||||||:||||||||:|||:| :| ||  | ||||
Db       1129 MKNLKKTSGVVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFGF 1188

Qy         61 QTFQPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDT 120
              ||||||| ||:||| | :| |||||||:||||| ||  |||||| ||||||||:||||||
Db       1189 QTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDGLLHYVSVISDN 1248

Qy        121 SGLRLLIDDQVLRRNQRLPSFSNAQQSLRLGGGHFEGCISNVLVQRFSQSPEVLDLASKS 180
              |||||||||||:|| ::||    |:::||||||| :|||||||| ||| | ||||||| | |
Db       1249 SGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNVFVQRLSLSPEVLDLTSNS 1308

Qy        181 TKKDASLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
              |:| |||||||||||||| |   |||| : | :|||
Db       1309 LKRDVSLGGCSLNKPPFLMLLKGSTRFNKTKTFRINQL 1346


RESULT 10
US-09-561-818A-12
; Sequence 12, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
;  APPLICANT: Kortesmaa, Jarrko
;  APPLICANT:  Tryggvason, Karl
;  TITLE OF INVENTION: Laminin 8 and Methods For Its Use
;  FILE REFERENCE: 99,274-D
;  CURRENT APPLICATION NUMBER: US/09/561,818A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 1792
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-561-818A-12

  Query Match             18.2%;  Score 204;  DB 4;  Length 1792;
  Best Local Similarity   29.1%;  Pred. No. 1.8e-14;
  Matches   64;  Conservative   35;  Mismatches   99;  Indels   22;  Gaps    8;

Qy          5 KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD-VPSTDRFQLSFGFQTF 63
              ||   ::   :|:||   | ||  : | |:  ||    ::  :   | |:  | |:|
Db       1180 KKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIASIQKISFFDGFEGGFNFRTL 1237

Qy         64 QPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHH-VSVISDTSG 122
              ||:| |  : : :    ::|::| : :  :   | :  :   | ||| |  |: ||||
Db       1238 QPNGLLFYYTSGSDVFSISLDNGTVVMDVK--GIKVMSTDKQYHDGLPHFVVTSISDTR- 1294

Qy        123 LRLLIDDQVLRRNQRLPSFSNAQQS------LRLGG-------GHFEGCISNVLVQRFSQ 169
                |::|   ||      |:   |:|:          ||          :| |||||    | :
Db       1295 YELVVDKSRLRGKN--PTKGKAEQTQTTEKKFYFGGSPISPQYANFTGCISNAYFTRLDR 1352

Qy        170 SPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 209
              || |    | |   ||  | :   |  :| |  |  :|
Db       1353 DVEVEDFQRYSEKVHTSLYECPIESSPLFLLHKKGKNSSK 1392


RESULT 11
US-09-561-818A-10
; Sequence 10, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
;  APPLICANT: Kortesmaa, Jarrko
;  APPLICANT:  Tryggvason, Karl
;  TITLE OF INVENTION: Laminin 8 and Methods For Its Use
;  FILE REFERENCE: 99,274-D
;  CURRENT APPLICATION NUMBER: US/09/561,818A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 1816
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-561-818A-10

  Query Match             18.2%;  Score 204;  DB 4;  Length 1816;
  Best Local Similarity   29.1%;  Pred. No. 1.9e-14;
  Matches   64;  Conservative   35;  Mismatches   99;  Indels   22;  Gaps    8;

Qy          5 KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD-VPSTDRFQLSFGFQTF 63
              ||   ::   :|:||   | ||  : | |:  ||    ::  :   | |:  | |:|
Db       1204 KKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIASIQKISFFDGFEGGFNFRTL 1261

Qy         64 QPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHH-VSVISDTSG 122
              ||:| |  : : :    ::|::| : :  :   | :  :   | ||| |  |: ||||
Db       1262 QPNGLLFYYTSGSDVFSISLDNGTVVMDVK--GIKVMSTDKQYHDGLPHFVVTSISDTR- 1318

Qy        123 LRLLIDDQVLRRNQRLPSFSNAQQS------LRLGG-------GHFEGCISNVLVQRFSQ 169
                |::|   ||      |:   |:|:          ||          :| |||||    | :
Db       1319 YELVVDKSRLRGKN--PTKGKAEQTQTTEKKFYFGGSPISPQYANFTGCISNAYFTRLDR 1376

Qy        170 SPEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 209
              || |    | |   ||  | :   |  :| |  |  :|
Db       1377 DVEVEDFQRYSEKVHTSLYECPIESSPLFLLHKKGKNSSK 1416
```

```
RESULT 12
US-09-561-818A-4
; Sequence 4, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
;  APPLICANT: Kortesmaa, Jarrko
;  APPLICANT:  Tryggvason, Karl
;  TITLE OF INVENTION: Laminin 8 and Methods For Its Use
;  FILE REFERENCE: 99,274-D
;  CURRENT APPLICATION NUMBER: US/09/561,818A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1792
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-561-818A-4

  Query Match             16.7%;  Score 187;  DB 4;  Length 1792;
  Best Local Similarity   28.3%;  Pred. No. 2e-12;
  Matches   62;  Conservative   34;  Mismatches  103;  Indels   20;  Gaps    8;

Qy          5 KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD-VPSTDRFQLSFGFQTF 63
              ||    ::   :|:||   | ||  : | | |:  ||    ::  :   | |:  | |:|
Db       1178 KKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIASIQKISFFDGFEGGFNFRTL 1235

Qy         64 QPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGL 123
              ||:| |  : : :    ::|::| : :  :   | :       | ||| |   |||  |
Db       1236 QPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQSVDKQYNDGLSHF--VISSVSPT 1291

Qy        124 R--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-------GHFEGCISNVLVQRFSQS 170
              |  |::|  :|  :|          | | :   ||         :| |||||    | :
Db       1292 RYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSPISAQYANFTGCISNAYFTRVDRD 1351

Qy        171 PEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 209
              || |    : |   ||  | :   | :| |  |  :|
Db       1352 VEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNLSK 1390


RESULT 13
US-09-561-818A-8
; Sequence 8, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
;  APPLICANT: Kortesmaa, Jarrko
;  APPLICANT:  Tryggvason, Karl
;  TITLE OF INVENTION: Laminin 8 and Methods For Its Use
;  FILE REFERENCE: 99,274-D
;  CURRENT APPLICATION NUMBER: US/09/561,818A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 1800
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-561-818A-8

  Query Match             16.7%;  Score 187;  DB 4;  Length 1800;
  Best Local Similarity   28.3%;  Pred. No. 2e-12;
  Matches   62;  Conservative   34;  Mismatches  103;  Indels   20;  Gaps    8;

Qy          5 KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD-VPSTDRFQLSFGFQTF 63
              ||    ::   :|:||   | ||  : | | |:  ||    ::  :   | |:  | |:|
Db       1178 KKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIASIQKISFFDGFEGGFNFRTL 1235

Qy         64 QPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGL 123
              ||:| |  : : :    ::|::| : :  :   | :       | ||| |   |||  |
Db       1236 QPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQSVDKQYNDGLSHF--VISSVSPT 1291

Qy        124 R--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-------GHFEGCISNVLVQRFSQS 170
              |  |::|  :|  :|          | | :   ||         :| |||||    | :
Db       1292 RYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSPISAQYANFTGCISNAYFTRVDRD 1351

Qy        171 PEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 209
              || |    : |   ||  | :   | :| |  |  :|
Db       1352 VEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNLSK 1390


RESULT 14
US-09-561-818A-2
; Sequence 2, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
;  APPLICANT: Kortesmaa, Jarrko
;  APPLICANT:  Tryggvason, Karl
;  TITLE OF INVENTION: Laminin 8 and Methods For Its Use
;  FILE REFERENCE: 99,274-D
;  CURRENT APPLICATION NUMBER: US/09/561,818A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1816
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-561-818A-2

  Query Match             16.7%;  Score 187;  DB 4;  Length 1816;
  Best Local Similarity   28.3%;  Pred. No. 2e-12;
  Matches   62;  Conservative   34;  Mismatches  103;  Indels   20;  Gaps    8;

Qy          5 KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD-VPSTDRFQLSFGFQTF 63
              ||    ::   :|:||   | ||  : | | |:  ||    ::  :   | |:  | |:|
Db       1202 KKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIASIQKISFFDGFEGGFNFRTL 1259

Qy         64 QPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGL 123
              ||:| |  : : :    ::|::| : :  :   | :       | ||| |   |||  |
Db       1260 QPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQSVDKQYNDGLSHF--VISSVSPT 1315

Qy        124 R--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-------GHFEGCISNVLVQRFSQS 170
              |  |::|  :|  :|          | | :   ||         :| |||||    | :
Db       1316 RYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSPISAQYANFTGCISNAYFTRVDRD 1375

Qy        171 PEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 209
              || |    : |   ||  | :   | :| |  |  :|
Db       1376 VEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNLSK 1414


RESULT 15
US-09-561-818A-6
; Sequence 6, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
;  APPLICANT: Kortesmaa, Jarrko
;  APPLICANT:  Tryggvason, Karl
;  TITLE OF INVENTION: Laminin 8 and Methods For Its Use
;  FILE REFERENCE: 99,274-D
;  CURRENT APPLICATION NUMBER: US/09/561,818A
;  CURRENT FILING DATE:  2000-04-28
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 1824
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-561-818A-6

  Query Match             16.7%;  Score 187;  DB 4;  Length 1824;
  Best Local Similarity   28.3%;  Pred. No. 2e-12;
  Matches   62;  Conservative   34;  Mismatches  103;  Indels   20;  Gaps    8;

Qy          5 KKTSGVVRLNDTVGVTKKCSEDWKLVRTASFSRGGQMSFTNLD-VPSTDRFQLSFGFQTF 63
```

```
                ||   ::   :|:||   | ||  : | | |:  ||    ::  :   | |:  | |:|
Db       1202 KKDFNLLEQTETLGVGYGCPEDSLISRRAYFN--GQSFIASIQKISFFDGFEGGFNFRTL 1259

Qy         64 QPSGTLLNHQTRTSSLLVTLEDGHIELSTRDSNIPIFKSPGTYMDGLLHHVSVISDTSGL 123
               ||:| |   : : :    ::|::| : :  :   | :      | ||| |   |||  |
Db       1260 QPNGLLFYYASGSDVFSISLDNGTVIMDVK--GIKVQSVDKQYNDGLSHF--VISSVSPT 1315

Qy        124 R--LLID-DQVLRRNQRLPSFSNAQQSLR---LGG-------GHFEGCISNVLVQRFSQS 170
               |  |::|  :|  :|          | | :    ||        :| |||||    |  :
Db       1316 RYELIVDKSRVGSKNPTKGKIEQTQASEKKFYFGGSPISAQYANFTGCISNAYFTRVDRD 1375

Qy        171 PEVLDLASKSTKKDASLGGCSLNKPPFLMLFKSPKRFNK 209
                || |    : |   ||  | :   |  :| |  |  :|
Db       1376 VEVEDFQRYTEKVHTSLYECPIESSPLFLLHKKGKNLSK 1414
```

Search completed: February 22, 2005, 08:40:56
Job time : 11.1795 secs